

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 264.351 Seconds
(without alignments)
5365.716 Million cell updates/sec

Title: US-09-300-482-1

Perfect score: 233

Sequence: 1 gttttgcagcttagtagaat.....ttgacaagggtattgttg 233

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	233	100.0	233	10	US-09-237-183A-1252
2	221.8	95.2	2311	18	US-10-425-115-160360
3	208.8	89.6	1770	18	US-10-425-115-160357
4	164.8	70.7	1693	18	US-10-437-963-23894
5	164.8	70.7	5580	18	US-10-437-963-91761
6	141	60.5	749	18	US-10-425-115-174626
7	138	59.2	713	18	US-10-767-701-12821
8	138	59.2	1929	18	US-10-425-115-48185
9	131.6	56.5	1924	18	US-10-739-930-5153
10	113.4	48.7	1900	18	US-10-437-963-509
11	113.4	48.7	2583	18	US-10-437-963-508

12	100.2	43.0	1844	17	US-10-425-114-9043	Sequence 9043, Ap
13	100.2	43.0	1854	17	US-10-425-114-29479	Sequence 29479, A
14	100.2	43.0	1947	17	US-10-424-599-81077	Sequence 81077, A
15	91.6	39.3	612	18	US-10-425-115-142724	Sequence 142724, A
16	87.2	37.4	2412	17	US-10-425-114-12043	Sequence 12043, A
17	87.2	37.4	2435	17	US-10-424-599-81074	Sequence 81074, A
18	82.2	35.3	1236	17	US-10-425-114-5220	Sequence 5220, Ap
19	82	35.2	666	18	US-10-767-701-10807	Sequence 10807, A
20	60.4	25.9	626	18	US-10-437-963-83072	Sequence 83072, A
21	42.8	18.4	105	18	US-10-425-115-60567	Sequence 60567, A
22	39	16.7	340	17	US-10-424-599-83608	Sequence 83608, A
23	35	15.0	402850	10	US-09-844-653-5	Sequence 5, Appl
24	34.6	14.8	672	17	US-10-282-122A-34479	Sequence 34479, A
25	34.4	14.8	10286	14	US-10-240-453-21	Sequence 13, Appl
26	34.4	14.8	10286	15	US-10-239-676-13	Sequence 21, Appl
27	34	14.6	649	13	US-10-027-632-139078	Sequence 139078, A
28	34	14.6	649	17	US-10-027-632-139078	Sequence 139078, A
29	33.6	14.4	23695	18	US-10-781-362-13	Sequence 13, Appl
30	33.6	14.4	23702	18	US-10-781-362-9	Sequence 9, Appl
31	33.6	14.4	23702	18	US-10-781-362-11	Sequence 11, Appl
32	33.6	14.4	23703	18	US-10-781-362-5	Sequence 5, Appl
33	33.6	14.4	23703	18	US-10-781-362-15	Sequence 7, Appl
34	33.6	14.4	23703	18	US-10-781-362-17	Sequence 15, Appl
35	33.6	14.4	23703	18	US-10-781-362-17	Sequence 17, Appl
36	33.6	14.4	23703	18	US-10-781-362-19	Sequence 19, Appl
37	32.4	13.9	233	18	US-10-425-115-172445	Sequence 172445, A
38	32.4	13.9	241	18	US-10-674-124A-23429	Sequence 23429, A
39	32.4	13.9	649	13	US-10-027-632-139077	Sequence 139077, A
40	32.4	13.9	649	17	US-10-027-632-139077	Sequence 139077, A
41	31.4	13.5	234	17	US-10-424-599-7634	Sequence 7634, Ap
42	31.4	13.5	13376	15	US-10-311-455-556	Sequence 556, App
43	31.2	13.4	454	10	US-09-918-995-29025	Sequence 29025, A
44	31.2	13.4	472	13	US-10-027-632-40743	Sequence 40743, A
45	31.2	13.4	472	17	US-10-027-632-40743	Sequence 40743, A

ALIGNMENTS

RESULT 1
US-09-237-183A-1252
; Sequence 1252, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dene K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 38-21 (15089)B
; CURRENT APPLICATION NUMBER: US/09/237.183A
; PRIOR FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 1252
; LENGTH: 233
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-1252

Query Match 100.0%; Score 233; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 6.4e-66;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTTGAGTAGTAGATATAGTGGCTCTATGATAGGTGGAAGATTGACTT 60
DB 1 GTTTTGAGTAGTAGATATAGTGGCTCTATGATAGGTGGAAGATTGACTT 60
QY 61 ATTGAATGAGCAATCTGAGTATGAGACTTCAGAAAAAATGATGAGGAGTACCG 120
DB 61 ATTGAATGAGCAATCTGAGTATGAGACTTCAGAAAAAATGATGAGGAGTACCG 120

[illegible]

```

RESULT 2
US-10-425-115-160360
; Sequence 160360, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ. ID NOS: 369326
; SEQ. ID NO 160360

```

```

; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: clone ID: MRT4577_77828C.1
US-10-425-115-160360

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Query Match	95.2%	Score 221.8;	DB 18;	Length 2311;
Best Local Similarity	97.0%;	Pred. No. 8.3e-62;		
Matches 226; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0.

1GTTTTGCAGTAGAGAAATGCTTAGTACGTGCTCCTATGATGATGGGTGGAAGATTTGACTT 60
585 GTTTTGCAGTTAGTAAATATGTTAGTGGCTCCATATATGGGTGGAAGATTTGAGTT 644
61 ATTGAATAGGCAATCTCTGAGTATGAGACTCAGAAAACAATGACTGGGAAGCTCCG 120
645 ATTAATATAGGCAATCTCTGAGTATGAACTTCAAAAACAATGACTGGGAAGCTCCG 704
121 CAGATTAATTTTATTTGGCATTGGCTCCATCAGTCTTACCATCAGTATCGAGATGATTAAG 180
705 CAGATTAATTTTATTTGGCATTGGCTCCATCAGTCTTACCATCAGTATCAGAAATGATTAAG 764
181 ATCATATTCAGTATGATCATCTTTCACACACCGGTTGGACAAGGCTTATTTGTTG 233
765 ATCATATTCAGTATGATCATCTTTCACACACCGGTTGGACAAGGCTTATTTGTTG 817

RESULT 3
JS-10-425-115-160357

PUBLICATION NO: US20040214272A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plasmids
 FILE REFERENCE: 38-21(5322)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO 160357

```

: LENGTH: 1770
: TYPE: DNA
: :
: ORGANISM: Zea mays
: FEATURE:
: :
: OTHER INFORMATION: Clone ID: MRT4577_77825C.1
: US-10-425-115-160357

```

Query Match	89.6%	Score 208.8;	DB 18;	Length 1770;
Best Local Similarity	96.8%;	Pred. No. 1.3e-57;		
Matches 213; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0

QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100																											
QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100																											
Db	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200												
QY	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200
Db	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177																																																																																															

RESULT 4
US-10-437-963-23894

```

1 // Sequence 23894, Application US/10437963
2 // Publication No. US20040123343A1
3 //
4 // GENERAL INFORMATION:
5 //
6 // APPLICANT: La Rosa, Thomas J.
7 // APPLICANT: Kovalic, David K.
8 // APPLICANT: Zhou, Yihua
9 // APPLICANT: Cao, Yongwei
10 // APPLICANT: Wu, Wei
11 // APPLICANT: Boukharov, Andrey A.
12 // APPLICANT: Barbazuk, Brad
13 //
14 // APPLICANT: Li, Ping
15 //
16 // TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
17 // FILE REFERENCE: 38-21(53221)B
18 // CURRENT APPLICATION NUMBER: US/10/437,963
19 // CURRENT FILING DATE: 2003-05-14
20 // NUMBER OF SEQ ID NOS: 204966
21 //
22 // SEQ ID NO 23894
23 //
24 // LENGTH: 1693
25 //
26 // TYPE: DNA
27 //
28 // ORGANISM: Oryza sativa
29 //
30 // FEATURE:
31 //
32 // OTHER INFORMATION: Clone ID: PAT_MRT4530_2892C.1
33 //
34 // US-10-437-963-23894

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Query Match	70.7%;	Score 164.8;	DB 18;	Length 1693;
Best local alignment:	01.00			

Matches 190; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

2	TTTTGGCAGTTAGTAGAATATGTTAGTGCCTCTATGATAGGGTGAAGCATTTGAGTTA	61
3	TTTTGGCAATTAATTAATAATATGTTAGTGTCTCTCAATAGCGGGGAAGATTTGCATCA	1011
4	TTGAAATGAGCAATCTCTGATGTGAGACTTCAAAAACAATGACTCGGGAAGCTACCGC	121
5	TTAAATACGCCCATTTACAGAGATGAACCTTGAGAAACAAACCAAGAAAGCTCAGCT	1071
6	AGATTTATTTATTTGGCATTTGCGCTCGATATGCTTCCCATCAAGTATGCGAATGATAAGA	181
7	AGACTATTTTATTTTGGCATTTGCGCTCCATCATAGCTTACCCCTCAGTATGCAAAATGATAGA	1131
8	TCATATTTGCATGATGCATCTTCACACACCGGTTGGACAAAGGTTATTTGTTG	233

DB 1132 TCATATGATGATGATTCATCTTCTCATCTGCGCTGAGCAAGGTTATTGTG 1183

RESULT 5
US-10-437-963-91761
; Sequence 91761, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 91761
; LENGTH: 5580
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_90304C.1
US-10-437-963-91761

Query Match 70.7%; Score 164.8; DB 18; Length 5580;
Best Local Similarity 81.9%; Pred. No. 5,9e-43;
Matches 190; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 2 TTTTGCAGTTAGTGAATATGTAGTGGCTCCTATGATGAGGCTGGAAGATTGAGTTA 61
DB 4117 TTTTGCATTTAATTAATATGTAGTGGCTCCTACAAATGCGGAGGAGATTGATCA 4176
QY 62 TTGAATGAGCAATCTCTGATGATGAGACTTCAGAAACATGACTCGGAAAGCTACCGC 121
DB 4177 TTAATTAAGCCATTTTCAGAGATGAACTTCGAGAGACAAACCAAGAGCTCAGCT 4236
QY 122 AGATTATTTATTTGGCATGCTGCCTCATGATCTACCCATCGATGCGAGATGATTA 181
DB 4237 AGACATATTTATTTGGCATGCTGCCTCATGATCTACCCCTCGATGCAAAATGATTA 4296
QY 182 TCATATTTGATGATGCTCATCTTCACACACCGGTTGGAAGAGGTTATTGTG 233
DB 4297 TCATATGATGATGATCTTCTCTCATTTGCTGCTGAGCAAGGTTATTGTG 4348

RESULT 6
US-10-425-115-174626
; Sequence 174626, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 174626
; LENGTH: 749
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_9083C.1
US-10-425-115-174626

Query Match 60.5%; Score 141; DB 18; Length 749;
Best Local Similarity 80.5%; Pred. No. 1.5e-35;
Matches 165; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 2 TTTTGCAGTTAGTGAATATGTAGTGGCTCCTATGATGAGGCTGGAAGATTGAGTTA 61
DB 545 TTTTGCATTTAATTAATATGTAGTGGCTCCTACAAATGCGGAGATTGATTA 604
QY 62 TTGAATGAGCAATCTCTGATGATGAGACTTCAGAAACATGACTCGGAAAGCTACCGC 121
DB 605 CTAAACAAGACATCTCTGAGATGAAACATCAGAGAAACCAACCAAGAAATCCCGA 664
QY 122 AGATTATTTATTTGGCATGCTGCCTCATGATCTACCCATCGATGCGAGATGATTA 181
DB 665 AGACATATTTATTTGGCATGCTGCCTCATGATCTACCCCTCGATGCAAAATGATTA 724
QY 182 TCATATTTGATGATGCTCATCTTCACACACCGGTTGGAAGAGGTTATTGTG 233
DB 725 TCATATTTGATGATCTCCTCTCTC 749

RESULT 7
US-10-767-701-12821
; Sequence 12821, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 12821
; LENGTH: 713
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS32515_1
US-10-767-701-12821

Query Match 59.2%; Score 138; DB 18; Length 713;
Best Local Similarity 78.0%; Pred. No. 1.4e-34;
Matches 181; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

QY 2 TTTTGCAGTTAGTGAATATGTAGTGGCTCCTATGATGAGGCTGGAAGATTGAGTTA 61
DB 390 TTTTGCATTTAATTAATATGTAGTGGCTCCTATGATGAGGAGGATTTCAGAA 449
QY 62 TTGAATGAGCAATCTCTGATGATGAGACTTCAGAAACATGACTCGGAAAGCTACCGC 121
DB 450 CTGAACAAGACATCTCTGAGATGAAACATCAGAGAAACCAACCAAGAAATCCCGA 503
QY 122 AGATTATTTATTTGGCATGCTGCCTCATGATCTACCCATCGATGCGAGATGATTA 181
DB 504 AGGCTCTTTATTTGGCATGCTGCCTCATGATCTACCCCTCGATGCAAAATGATTA 563
QY 182 TCATATTTGATGATGCTCATCTTCACACACCGGTTGGAAGAGGTTATTGTG 233
DB 564 ACATATTTGATGATGATCTTCTCTCATCTGCTGAGCAAGGTTATTGTG 615

RESULT 8
US-10-425-115-48185
; Sequence 48185, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua


```

: CURRENT FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 204966
: SEQ ID NO 508
: LENGTH: 2583
: TYPE: DNA
: ORGANISM: Oryza sativa
: FEATURE:
: OTHER INFORMATION: Clone ID: PAT_MRT4530_100463C.1
: US-10-437-963-508

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Query Match	48.7%;	Score 113.4;	DB 18;	Length 2583;
Best Local Similarity	75.1%;	Pred. No. 2.9e-26;		
Matches 157;	Conservative 0;	Mismatches 46;	Indels 6;	Gaps 1.

Qy	TTTTTGAGATTAGATATGTTAATGGCTCTATGAGTATGGGTGAGAGATTGAGTAA	61	APPLICANT: Cao, Yongwei
2	TTTTTGAGATTAGATATGTTAATGGCTCTATGAGTATGGGTGAGAGATTGAGTAA		TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
1453	TTTTTGCAACATTTAAATAATGTCATGAGTCTCTATGACAGCGGAGAGAGATTTGAGAAA	1512	TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
Db	TTTTTGCAACATTTAAATAATGTCATGAGTCTCTATGACAGCGGAGAGAGATTTGAGAAA		TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

Dy 62 TTGATATAGGCCAATCTGTAGTATGACCTCAGAAACAATGCCTGGGAAGCTAACCC 121
 ||||| ||||| |||||
Db 1513 TTGCAACAAGAAATTTCAGAGTATGGAAGTCA-----AACCAATCAGAAAAGCCCTCGC 156
 ||||| ||||| |||||

Qy 122 AGATTATTTATTTGGCATTGCCCTCCATCAGTCAACCATCAGATGCGAGATGTAAGA 181

Db 1567 AGGCTCTTCTATTGGCATTCGCTCCATCTGTCTAACCTTCAGTCTGCAAATATGATCAGA 1622

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QY      182 TCATATTGCATGAGTCCATCTTCACACAC 210
          |||||
Db      1627 ACATATTGCATGAATCCATCTGATGAC 1655

```

RESULT 12
US-10-425-114-9043

? APPLICANT: Liu, Jingdong
 ? APPLICANT: Zhou, Yihua
 ? APPLICANT: Kovalic, David K.
 ? APPLICANT: Screen, Steven E.
 ? APPLICANT: Tabaska, Jack E.
 ? APPLICANT: Cao, Yongwei
 ? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

OTHER INFORMATION: Clone ID: 700832220_FLL
US-10-425-114-9043

Query Match	43.0%	Score 100.2	DB 17	Length 1844
Best Local Similarity	64.4%	Pred. No. 5.3e-22		
Matches 150, Conservative	0	Mismatches 83	Indels 0	Gaps 0

QY 1 GTTTTGGCATTAGTAATATGTTAGTGCGCTCCATGATAGGGGTGAAGAATTGAGTT 60
|||||
Db 400 GTTTTACAGCTGATCAAAATATGTAAGCGGCTTATGATTC TGAGGATGCGTTCCGCGCT 459

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Oy      61  ATTGAATGAGGCAATCTCTGATATAGACTTCAGAAAACAATGACTCGGGAAGCTACCG 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      460  GTTGATTAAGAGATTTCAAGCATCATATATTGAAAAACAAGTTGAGGGTTATCTCG 519

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db 520 GAGGCTTTCTATCTTGCTCTTCCACCTTCAGTATATCCATCAGTTTGCAAGATGAT
QY 181 ATCATATTGCATGAGTCCATCTTCACACACCGGTTGGACAAAGGTTATTGTTG 233

Db 580 GACTTGTTCATGATAATCTGATCTTGGTGATGACACGGCTTGTGTTG 632

RESULT 13
US-10-425-114-29479
Source 28479 2011cat:cn US/10425114

APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
INVENTOR: 30 31/07/2010

OTHER INFORMATION: Clone ID: UC-GMFLMINSOY050C02_F111
US-10-425-114-29479

Query Match	43.0%	Score 100.2;	DB 17;	Length 1854;
Best Local Similarity	64.4%	Pred. No. 5.3e-22;		
Matches 150;	Conservative 0;	Mismatches 83;	Indels 0;	Gaps 0

Qy 1 GTTTTGAGTTCATGATATCTTAGTGGCTCCATGATAGGGGTGAAGATTGACTT 60
| | | | | | | | | | | | | | | | | | | | |
Db 410 GTTTTACAGCTGATCAAAATATGTAAGCGGCTTTATGATCTGAGGATGGCTTCCGCCT 469

Dy 61 ATTGAATGAGGCATCTCGAGTATGAGACTTCAGAAAAACATGACTCGGGAAGCTAACCG 120

Dd 470 GTTGAGATAAAGAGATTTCAGAGCATGAAATATTTGAAAAACAAGTGTGAGGGTTTATCTCG 529

Qy 121 CAGATTATTTATTTGGCATTGCTCCATAGTCAACCATCAGTATGCAGATGATTAAG 180
Db 530 GAGGCTTTCTACTTGTGCTTCCACCTTCAGTATATCCATCAGTTTGCAAGATGATCAA 589

Publication No. US20040031072A1
; GENERAL INFORMATION:

APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21 (53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ. ID NOS: 285684
 SEQ. ID NO 81077

Query Match 43.0%; Score 100.2; DB 17; Length 1947;
Best Local Similarity 64.4%; Pred. No. 5.4e-22;
Matches 150; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

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QY 1 GTTTTGCACTTAGTAGAATATGTTAGTGGCTCCTATGATAGGGTGAAGATTGAGTT 60
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Db 481 GTTTTACAGCTGATCAAAATATGTAAGCGGCTCTTATGATTCGAGGATGGCTCCGCT 540
    |||||
QY 61 ATTGAATGAGGCAATCTCTAGATAGACTTCAGAAAACAATGACTCGGGAAGCTACCG 120
    |||||
Db 541 GTTGGATTAAGAGATTCAAGCATGAATATTGAAAAACAGTTTGAGGGTTATCTCG 600
    |||||
QY 121 CAGATTATTTTATTTGGCATTTGCCATCAGTCTACCCAGTATGAGATGATTAAG 180
    |||||
Db 601 GAGGCTTTCTATCTGCTCTTCCACCTTCAATATCCATCAGTTTGCAAGATGATCAA 660
    |||||
QY 181 ATCAATATTCATGATGATTCATCTTCACACACCGGTTGACAGAGGTTATTGTTG 233
    |||||
Db 661 GACTGTGTCATGAATAAATCTGATCTTGATGATGACACGTGTTGTTGTTG 713
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RESULT 15

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US-10-425-115-142724
; Sequence 142724, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 142724
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_61645C.1
US-10-425-115-142724
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Query Match 39.3%; Score 91.6; DB 18; Length 612;
Best Local Similarity 74.4%; Pred. No. 2.1e-19;
Matches 131; Conservative 0; Mismatches 39; Indels 6; Gaps 1;

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QY 2 TTTTGGCACTTAGTAGAATATGTTAGTGGCTCCTATGATAGGGTGAAGATTGAGTTA 61
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Db 440 TTCTTGCAATTGATTAATAATATGTCAGTGGTCTCTATGACGGGAGAAAAGTTGAAAA 499
    |||||
QY 62 TTGAATGAGGCAATCTCTGAGATAGACTTCAGAAAACAATGACTCGGGAAGCTACCGC 121
    |||||
Db 500 CTGAACAAGGAATATCAGATTATGAGATGTC-----CAACAACCTCGGGAATCTCCGC 553
    |||||
QY 122 AGATTATTTTATTTGGCATTTGCCATCAGTCTACCCAGTATGAGATGAT 177
    |||||
Db 554 AGGCTATTTTATTTGGCATTTGCCATCTGTTTACCTTCACTGGGCAAAATGAT 609
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Search completed: May 4, 2005, 21:11:26
Job time : 266.351 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 76.9588 Seconds
(without alignments)
5591.830 Million cell updates/sec

Title: US-09-300-482-4

Perfect score: 263
Sequence: 1 gaagcacttttgatgtgc.....agungnactnnnnnganna 263

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.4	23.3	1830121	4 US-09-557-884-1	Sequence 1, Appli
2	61.4	23.3	1830121	4 US-09-643-990A-1	Sequence 1, Appli
3	59.6	22.7	6132	4 US-09-809-665A-7	Sequence 7, Appli
4	58.2	22.1	1533	4 US-09-134-000C-2369	Sequence 2369, Ap
5	54	20.5	3015	4 US-09-710-279-3401	Sequence 3401, Ap
6	54	20.5	3081	4 US-09-710-279-3602	Sequence 3602, Ap
7	52	19.8	1548	4 US-09-107-532A-1949	Sequence 1949, Ap
8	51.4	19.5	1692	4 US-08-956-121E-53	Sequence 53, Appli
9	51.4	19.5	1692	4 US-08-781-986A-53	Sequence 53, Appli
10	50.6	19.2	2494	3 US-08-714-918-3	Sequence 3, Appli
11	50.6	19.2	2494	3 US-09-265-315-3	Sequence 3, Appli
12	50.6	19.2	2494	3 US-09-265-315-3	Sequence 3, Appli
13	50.6	19.2	2494	3 US-09-266-417-3	Sequence 3, Appli
14	50.6	19.2	2494	4 US-09-527-745-3	Sequence 3, Appli
15	50.6	19.2	2494	4 US-09-527-745-3	Sequence 3, Appli
16	49.6	18.9	1488	3 US-08-962-859A-1	Sequence 1, Appli
17	49.6	18.9	1488	4 US-09-583-110-1905	Sequence 1905, Ap
18	49.6	18.9	1488	4 US-09-107-433-785	Sequence 785, App
19	49	18.6	669	4 US-09-902-540-1996	Sequence 1996, Ap
20	49	18.6	720	4 US-09-902-540-4	Sequence 4, Appli
21	48.2	18.3	744	4 US-09-248-796A-3185	Sequence 3185, Ap
22	48	18.3	2764	2 US-08-986-963-4	Sequence 4, Appli
23	48	18.3	13121	2 US-08-961-527-126	Sequence 126, App
24	47.2	17.9	640681	4 US-09-790-988-1	Sequence 1, Appli
25	45.2	17.2	1554	3 US-09-134-001C-351	Sequence 351, App
26	44.6	17.0	219	3 US-09-134-001C-1197	Sequence 1197, Ap
27	42.6	16.2	2631	4 US-09-949-016-4987	Sequence 4987, Ap

28	42	16.0	3376	4 US-09-710-279-4055	Sequence 4055, Ap
29	39.6	15.1	6995	4 US-09-531-26C-1	Sequence 1, Appli
30	37.4	14.2	1461	3 US-08-445-463B-5	Sequence 5, Appli
31	37.4	14.2	1461	3 US-08-445-464C-5	Sequence 5, Appli
32	37.4	14.2	1461	3 US-08-044-857D-5	Sequence 5, Appli
33	37.4	14.2	1461	5 PCT-US94-03437-5	Sequence 5, Appli
34	37.2	14.1	1455	5 PCT-US94-03437-7	Sequence 7, Appli
35	37.2	14.1	1467	5 PCT-US94-03437-3	Sequence 3, Appli
36	37.2	14.1	1571	3 US-08-445-463B-3	Sequence 3, Appli
37	37.2	14.1	1571	3 US-08-445-464C-3	Sequence 3, Appli
38	37.2	14.1	1571	3 US-08-044-857D-3	Sequence 3, Appli
39	37.2	14.1	1696	1 US-07-737-071A-1	Sequence 1, Appli
40	37.2	14.1	1696	1 US-08-022-096-1	Sequence 1, Appli
41	37.2	14.1	1696	3 US-08-445-463B-7	Sequence 7, Appli
42	37.2	14.1	1696	3 US-08-445-464C-7	Sequence 7, Appli
43	37.2	14.1	1696	3 US-08-044-857D-7	Sequence 7, Appli
44	36.4	13.8	34266	4 US-09-949-016-13250	Sequence 13250, A
45	36.2	13.8	2853	4 US-09-620-312D-463	Sequence 463, App

ALIGNMENTS

RESULT 1
US-09-557-884-1/c
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
Query Match 23.3%; Score 61.4; DB 4; Length 1830121;
Best Local Similarity 52.1%; Pred. No. 1.3e-08;
Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
53 AGGATGGAATGCAATATATTGGAGAGCCATTGGCTTGATGCACCTTTCTTCCCATTA 112

Db 577356 ATGGCTGAAAACGTTATTCGTTGAAAAAAGCTTTGGTTAGAGAAAAAAGCGGCAAA 577297
Qy 113 GGCTGACAAATATCTCTTTCAAACTTTCAGAAAAAGCAATATATAGATTGANCATC 172
Db 577296 CATTAGACGTACAAATCCACCGCTTCTTTGAAAGAACCAAAATTTATCGTATGATCAT 577237
Qy 173 TACTAGAGAAGAAATCAGTAAATAATCCATCAGGTTTAAAGGTTTCAANNAGNTTTTG 232
Db 577236 ATTTAGGTAAAGAAACCGTTCAAAACTTGCTCGTATTAAGTTTCAAAATGGTTGGTTG 577177
Qy 233 AGCCACCTTNGAGNNGNACNTNNNNGANA 263
Db 577176 AACCGCTTGGAAACGTAATTCATTGATTA 577146

RESULT 2

US-09-643-990A-1/c
Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Pleischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match 23.3%; Score 61.4; DB 4; Length 1830121;
Best Local Similarity 52.1%; Pred. No. 1.3e-08;
Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
Qy 53 AGGATGCAATCGATATATTTGAGAGCCATTGGCTTGATGACATTTCTTCCATA 112

Db 577356 ATGGCTGAAAACGTTATTCGTTGAAAAAAGCTTTGGTTAGAGAAAAAAGCGGCAAA 577297
Qy 113 GGCTGACAAATATCTCTTTCAAACTTTCAGAAAAAGCAATATATAGATTGANCATC 172
Db 577296 CATTAGACGTACAAATCCACCGCTTCTTTGAAAGAACCAAAATTTATCGTATGATCAT 577237
Qy 173 TACTAGAGAAGAAATCAGTAAATAATCCATCAGGTTTAAAGGTTTCAANNAGNTTTTG 232
Db 577236 ATTTAGGTAAAGAAACCGTTCAAAACTTGCTCGTATTAAGTTTCAAAATGGTTGGTTG 577177
Qy 233 AGCCACCTTNGAGNNGNACNTNNNNGANA 263
Db 577176 AACCGCTTGGAAACGTAATTCATTGATTA 577146

RESULT 3

US-09-809-665A-7
Sequence 7, Application US/09809665A
Patent No. 6790950
GENERAL INFORMATION:
APPLICANT: Lowery E., David, et al.
TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
FILE REFERENCE: 28341/00435
CURRENT APPLICATION NUMBER: US/09/809,665A
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/153,453
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/126,689
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 09/545,199
NUMBER OF SEQ ID NOS: 2000-04-06
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 6132
TYPE: DNA
ORGANISM: Pasteurella multocida
FEATURE:
NAME/KEY: CDS
LOCATION: (4032)..(4727)
OTHER INFORMATION: devB
US-09-809-665A-7

Query Match 22.7%; Score 59.6; DB 4; Length 6132;
Best Local Similarity 51.4%; Pred. No. 3.5e-09;
Matches 110; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
Qy 50 AGAAGGATGAATCGCATATATTTGAGAGCCATTGGCTTGTGATGACATTTCTTCCC 109
Db 2903 AGTTGGCTGGAAGCGTTATTTGTGAAAAACCGTTTGGTTATGATATACGACGCA 2962
Qy 110 ATAGGCTGACATATCTCTTTCAAACTTTCAGAAAAAGCAATATATAGATTGANC 169
Db 2963 AAGAACTCGATATTCAAATTCACCGTTCTTGATGAAACCAAAATTTATCGATTGACC 3022
Qy 170 ATCTACTAGGAAGAAATCAGTAAATAATCCATCAGGTTTAAAGGTTTCAANNAGNTT 229
Db 3023 ACTATCTTGTAAAGAAACCGTTCAAAATCTGCTGTGTGCTGTTTCTAATGATGCT 3082
Qy 230 TTGAGCCACCTTNGAGNNGNACNTNNNNGANA 263
Db 3083 TTGAACCACTCTGGAACCGTAATTCATTGATTA 3116

RESULT 4

US-09-134-000C-2369
Sequence 2369, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032

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CURRENT APPLICATION NUMBER: US/09/134,000
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2369
LENGTH: 1533
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-2369

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Query Match	22.1%;	Score 58.2;	DB 4;	Length 1533;
Best Local Similarity	51.2%;	Pred. No. 5.3e-09;		
Matches 108; Conservative	0;	Mismatches 103;	Indels 0;	Gaps 0

QY 113 GCGTCACAAATATCTTTCTTTCAAACTTTCAGGAAAGCAAAATATATAGAAITGANCATC 172
 Db 425 AAGGCTTTGATCGTCTAATATATCGAAAAGCCATTGGTTCGATTATAGAAATCTGCCACG 484
 QY 5 AGGGATGGAATGCGATAATATATTTGGAAGCCATTGGCTTGAATGCACTTCTTCCCATTA 112
 QY 173 TACTAGGAAGGAATCNCAGTAAATCTCINAGGTTTAAGGTTTCAANNAGTTTTG 232
 Db 545 ACTTGGGCAAGAAATGATGCCAAAATATTTTTCAGCCATTGTTTTGCCAATATATATTTTG 604
 QY 233 AGGCACCTTNGAGNNGNACNTNNNNNGANNA 263
 Db 605 AATCACATGGAACAATCGTTACATTGATAA 635

RESULT 5
US-09-710-279-3401

```

1  APPLICANT:KIMBERLY, WILLIAM JOHN
2  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
3  FILE REFERENCE: PUS480US
4
5  CURRENT APPLICATION NUMBER: US/09/710.279
6  CURRENT FILING DATE: 2000-11-09
7  PRIOR APPLICATION NUMBER: 60/164,258
8  PRIOR FILING DATE: 1999-11-09
9  NUMBER OF SEQ ID NOS: 4472
10 SOFTWARE: PatentIn Ver. 2.1
11 SEQ ID NO 3401
12     LENGTH: 3015
13     TYPE: DNA
14     ORGANISM: Artificial Sequence
15     FEATURE:
16     OTHER INFORMATION: Description of Artificial Sequence: synthetic
17     OTHER INFORMATION: nucleic acid sequence
18     IS-09-710-279-3401

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Query Match	20.5%	Score 54;	DB 4;	Length 3015;
Best Local Similarity	54.5%;	Pred. No. 1.8e-07;		
Matches 114;	Conservative 0;	Mismatches 93;	Indels 2;	Gaps 1

QY	45	GACCCAGAAAGGATGGAAATCCCAATAAATTTGAGAAGCATTTGGCTTTGAATGACATTTTC	104
Db	1315	GAACTGTAAGGAGGGGTGATGCCAATATATATATGAAAAACCATTTGGTGATGATTTAAATTC	1374
QY	105	TTCCCATAGGCTGACACAAATATCTTCTTCCAACTTTCAGAAAAAGCAAAATATATGAAT	164
Db	1375	T--GCCAAAAATTTAAATATCAAAATAGAAAAGTCTTTTAGAGAGAAAAATATTTGGAAAT	1433
QY	165	TGANCATCTACAGGAAGGAATCNCAGTAAAAATCTCNCAGTTTAAAGGTTTCAANNN	224
Db	1433	TGATCACAATTTAGGTAAAGAAATGATTCAAAAATATTAAGTCTACAGTTTTTGAACAC	1499
QY	225	AGATTTTGAGCCACCTTNGAGNNGNACAT	253

Db 1493 TATATTGAACCACTTGAATAATAAGT 1521

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RESULT 6
US-09-710-279-3602/c
: Sequence 3602, Application US/09710279
: Patent No. 6703492
: GENERAL INFORMATION:
: APPLICANT: KIMMERLY, WILLIAM JOHN
: TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
: FILE REFERENCE: PU3480US
: CURRENT APPLICATION NUMBER: US/09/710,279
: CURRENT FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: 60/164,258
: PRIOR FILING DATE: 1999-11-09
: NUMBER OF SEQ ID NOS: 4472
: SOFTWARE: PatencIn Ver. 2.1
: SEQ ID NO 3602
: LENGTH: 3081
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: synthetic
: OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3602

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Query Match	20.5%;	Score 54;	DB 4;	Length 3081;
Best Local Similarity	54.5%;	Pred. No. 1.8e-07;		
Matches 114;	Conservative 0;	Mismatches 93;	Indels 2;	Gaps 1

QY	105	TTCCCATAGGCTGACACAATATCTTTCTTCAAACTTTGACGAAAGCAAAATATATAGAT	164
Db	2286	T--GCAAAATAATTAAATTAATCAATAAGAAAGCTCTTTAAGAGAAAAAATAATTGGAAAT	2229
QY	165	TGANCATCTACTTGTGGAAGGAATCNCAGTNAAAATCCATCAGGTTTAAGGGTTCAANNNN	224
Db	2228	TGATCACTATTTTTGTGTAAAGAAATGATTTCAAAATATTGAACGCTTCAGATTTTGAAACAC	2169
QY	225	AGNTTTTGAGCCACCTTGAGNNGNACNT	253
Db	2168	TATATTTTGAACCACTTTGGAAATATATAGT	2140

RESULT 7
 US-09-107-532A-1949
 Sequence 1949, Application US/09107532A
 Patent No. 6583275
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02354
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: CTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1949:
SEQUENCE CHARACTERISTICS:
LENGTH: 1548 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1548
SEQUENCE DESCRIPTION: SEQ ID NO: 1949:
US-09-107-532A-1949

Query Match 19.8%; Score 52; DB 4; Length 1548;
Best Local Similarity 48.3%; Pred. No. 5.9e-07;
Matches 112; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
QY 32 CAAGCAGTCTGACCCAGAGAGATGATGATATATTGAGAGCCATTGGCT 91
DB 419 CCAAAATATATATGACAAAATATGCTTCATGTTGATGATGAAAAACCGTTG 478
QY 92 TTGATGACATCTTCTCCCAATAGCTGACACATATCTTTTCAACCTTCAGAAAAGC 151
DB 479 CTGATACCAAGTCTGTTTGAATGAAACGACCAATCAGAGAATATCCAGAAACAG 538
QY 152 AATATATATGAAATGATGATCTACTAGAAAGATCNCAGTNAATCCTNAGAGTTTAA 211
DB 539 ATATTTTTCAGATTTGATATTTATTTAGAAAAAATGATCCAAACATCTCAGCTATCC 598
QY 212 GGGTTTCAANNAGTTTTTGAGCCACTTNGAGNNAGNCTNNNNNGANNA 263
DB 599 GTTTGCCAATAATATTTTGAAGGCTCAATGGAACAATCGTATATCGCAA 650

RESULT 8

US-08-956-171E-53
Sequence 53, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 16592 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-08-956-171E-53

Query Match 19.5%; Score 51.4; DB 4; Length 16592;
Best Local Similarity 51.0%; Pred. No. 2.8e-06;
Matches 103; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 52 AAGGATGGAATCCGATATATTTGAGAGCATTGGCTTGAATGACATTTCTCCAT 111
DB 814 AAAGATTTAAAGCTGTTTATGAAAAACCATTCGTAGTATTAATCAGCCGA 873
QY 112 AGCTGACACATATCTTCTTCAACTTCAGAAAAAGCAATATATGATGATGAT 171
DB 874 GCATTAACAATCAATTCGTAATTCATTTAAGAAAGAAATTTATCGTATGACAC 933
QY 172 CTACTAGGAAGAAATCNCAGTNAATCCTNAGGTTTAAAGGTTTCAANNAGTTTT 231
DB 934 TATTAGAAAAGCATGTTTCAAAATATCAGAGTATTCGTTTGGCAATGGAGTTT 993
QY 232 GAGCAGCTTNGAGNNAGNCT 253
DB 994 GAACCATTTATGATATACAAAT 1015

RESULT 9

US-08-781-986A-53
Sequence 53, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Bob
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PB248BP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16592 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-781-986A-53

Query Match 19.5%; Score 51.4; DB 4; Length 16592;
 Best Local Similarity 51.0%; Pred. No. 2.8e-06;
 Matches 103; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 52 AAGGATGGAATCGATATATTGAGAGCCATTGGCTTGATGCACTTCTTCCAT 111
 DB 814 AAGGATTTAAACGCTTGTATCGAAAAACATTGCGTAGTATTTAAATCAGCCGAA 873
 QY 112 AGCGTACACATATCTTCTTCAACTTCAGSAAAGCAATATATGATGANCAT 171
 DB 874 GCATTAAACATCAATTCGTAATCATTTAAAGAAAGAAATTTATCGATGACAC 933
 QY 172 CTACTAGAGAGATCNCAGTAAATCCTTCAGGTTTAAGGTTTCAANNAGTTT 231
 DB 934 TATTAGGAAAGACATGTTTCAAAATATCGAGTATTACGTTTGGCAATCGATGTT 993
 QY 232 GAGCCACCTTGAGNNAACNT 253
 DB 994 GAACCATTAATGAAATTAACAAT 1015

RESULT 10
 US-08-714-918-3/c
 Sequence 3, Application US/08714918
 Patent No. 6037123

GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ving
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
 TITLE OF INVENTION: TARGET GENES
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/714,918
 FILING DATE: September 13, 1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 222/005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2494 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-714-918-3

Query Match 19.2%; Score 50.6; DB 3; Length 2494;
 Best Local Similarity 50.0%; Pred. No. 2.1e-06;
 Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

QY 52 AAGGATGGAATCGATATATTGAGAGCCATTGGCTTGATGCACTTCTTCCAT 111
 DB 1425 AAGGATTTAAACGCTTGTATCGAAAAACATTGCGTAGTATTTAAATCAGCCGAA 1366
 QY 112 AGCGTACACATATCTTCTTCAACTTCAGSAAAGCAATATATGATGANCAT 171
 DB 1365 GCATTAAACATCAATTCGTAATCATTTAAAGAAAGAAATTTATCGATGACAC 1306
 QY 172 CTACTAGAGAGATCNCAGTAAATCCTTCAGGTTTAAGGTTTCAANNAGTTT 231
 DB 1305 TATTAGGAAAGACATGTTTCAAAATATCGAGTATTACGTTTGGCAATCGATGTT 1246
 QY 232 GAGCCACCTTGAGNNAACNT 253
 DB 1245 GAACCATTAATGAAATTAACAAT 1224

RESULT 11
 US-09-265-315-3/c
 Sequence 3, Application US/09265315
 Patent No. 6187541

GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ving J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-3

Query Match 19.2%; Score 50.6; DB 3; Length 2494;
Best Local Similarity 50.0%; Pred. No. 2.1e-06;
Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

QY 52 AAGGATGGAATGCAATATATTGAGAGCCATTGGCTTGATGACCTTTCTCCCAT 111
DB 1425 AAGGATTTAAAGCCTGTGATGAAAAACATTCGTAGTATTTAAATCAGCCGAA 1366
QY 112 AGGCTGACACATATCTTCTTCAAACTTCAGAAAAACAATATATGAAATTGANCAT 171
DB 1365 GCATTAAACAATCAATTCGTAATCATTTAAAGAAAGAAATTAATGATGACCCAC 1306
QY 172 CTACTAGAGAGATCNCAGTNAATCTTCAGGTTTAAGGTTTCAANNAGNTTT 231
DB 1305 TATTAGAAAAAGCATGTTCAAAATATGAGAGTATTACGTTTGCATGCGATGTT 1246
QY 232 GAGCCACCTTNGAGNNAGNCAT 253
DB 1245 GAACCATTTATGAAATTAACAAT 1224

RESULT 12
US-09-265-315-3/c
Sequence 3, Application US/09265315
Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315

FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-3

Query Match 19.2%; Score 50.6; DB 3; Length 2494;
Best Local Similarity 50.0%; Pred. No. 2.1e-06;
Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

QY 52 AAGGATGGAATGCAATATATTGAGAGCCATTGGCTTGATGACCTTTCTCCCAT 111
DB 1425 AAGGATTTAAAGCCTGTGATGAAAAACATTCGTAGTATTTAAATCAGCCGAA 1366
QY 112 AGGCTGACACATATCTTCTTCAAACTTCAGAAAAACAATATATGAAATTGANCAT 171
DB 1365 GCATTAAACAATCAATTCGTAATCATTTAAAGAAAGAAATTAATGATGACCCAC 1306
QY 172 CTACTAGAGAGATCNCAGTNAATCTTCAGGTTTAAGGTTTCAANNAGNTTT 231
DB 1305 TATTAGAAAAAGCATGTTCAAAATATGAGAGTATTACGTTTGCATGCGATGTT 1246
QY 232 GAGCCACCTTNGAGNNAGNCAT 253
DB 1245 GAACCATTTATGAAATTAACAAT 1224

RESULT 13
US-09-266-417-3/c
Sequence 3, Application US/09266417
Patent No. 6228588
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ying J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-266-417-3

Query Match 19.2% Score 50.6; DB 3; Length 2494;
Best Local Similarity 50.0%; Pred. No. 2.1e-06;
Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

52 AAGGATGGAATCGATATATTTGAGAAGCATTGGCTTGATGCACTTTCTCCCAT 111
1425 AAAGATTAAACGCTTGTATCGAAAACCATTCGGTAGTGATTTAAATCAGCCGAA 1366

112 AGCGTACACATATCTTCTTCAAACTTCAGAGAAAGCAATATATGATGANCAT 171
1365 GCATTAAACAATCAATTCGTAATCATTTTAAAGAAAGAAATTTAYCGTATKACAC 1306

172 CTACTAGAGAGAAATCNCAGTNAAAATCCTNCAGGTTTAAGGTTTCAANNAGTTT 231
1305 TATTTAGAGAAAAGACATGTTCAAAATATCGAGTATTTAGTTTGGCATGCGATGTTT 1246

232 GAGCCACCTTNGAGNNGACNT 253
1245 GAACCATATGGAATTAACAAT 1224

RESULT 14
US-09-528-709-3/c
Sequence 3, Application US/09528709
Patent No. 6630303
GENERAL INFORMATION:
APPLICANT: Benton, Bret
Lee, Ving
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,709
FILING DATE: 17-Mar-2000
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-528-709-3

Query Match 19.2% Score 50.6; DB 4; Length 2494;
Best Local Similarity 50.0%; Pred. No. 2.1e-06;
Matches 101; Conservative 2; Mismatches 99; Indels 0; Gaps 0;

52 AAGGATGGAATCGATATATTTGAGAAGCATTGGCTTGATGCACTTTCTCCCAT 111
1425 AAAGATTAAACGCTTGTATCGAAAACCATTCGGTAGTGATTTAAATCAGCCGAA 1366

112 AGCGTACACATATCTTCTTCAAACTTCAGAGAAAGCAATATATGATGANCAT 171
1365 GCATTAAACAATCAATTCGTAATCATTTTAAAGAGAGAAATTTATCGTATKACAC 1306

172 CTACTAGAGAGAAATCNCAGTNAAAATCCTNCAGGTTTAAGGTTTCAANNAGTTT 231
1305 TATTTAGAGAAAAGACATGTTCAAAATATCGAGTATTTAGTTTGGCATGCGATGTTT 1246

232 GAGCCACCTTNGAGNNGACNT 253
1245 GAACCATATGGAATTAACAAT 1224

RESULT 15
US-09-527-745-3/c
Sequence 3, Application US/09527745
Patent No. 6638718
GENERAL INFORMATION:
APPLICANT: Benton, Bret
Lee, Ving
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles

```

1 STATE: California
2 COUNTRY: U.S.A.
3 ZIP: 90071-2066
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
7
8 Storage
9
10 COMPUTER: IBM Compatible
11 OPERATING SYSTEM: IBM P.C. DOS 5.0
12 SOFTWARE: Word Perfect 5.1
13
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/09/527,745
16 FILING DATE: 17-Mar-2000
17
18 CLASSIFICATION: 424
19
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US/08/714,918
22 FILING DATE: September 13, 1996
23 APPLICATION NUMBER: 60/009,102
24 FILING DATE: December 22, 1995
25 APPLICATION NUMBER: 60/003,798
26 FILING DATE: September 15, 1995
27
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Warburg, Richard J.
30 REGISTRATION NUMBER: 32,327
31 REFERENCE/DOCKET NUMBER: 222/005
32
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (213) 489-1600
35 TELEFAX: (213) 955-0440
36
37 TELEX: 67-3510
38
39 INFORMATION FOR SEQ ID NO: 3:
40
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 2494 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46
47 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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49 US-09-527-745-3
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Search completed: May 4, 2005, 12:27:36
Job time : 81.9588 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 298.387 Seconds
(without alignments)
5365.716 Million cell updates/sec

Title: US-09-300-482-4
Perfect score: 263
Sequence: 1 gaagcactttggatgtgc.....agmgnacntnnnnnganna 263

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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2:	/cgn2_6/ptodata/1/pubpna/ECT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
5:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
6:	/cgn2_6/ptodata/1/pubpna/ECTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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16:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18:	/cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	235	89.4	1680	17	US-10-425-114-8171
2	235	89.4	2218	17	US-10-424-599-48573
3	215.2	81.8	237	10	US-09-237-183A-2682
4	175.8	66.8	260	10	US-09-237-183A-2684
5	123.2	46.8	2218	18	US-10-437-963-65487
6	71.8	27.3	1577	17	US-10-424-599-3107
7	64.2	24.4	1482	17	US-10-282-122A-9984
8	61.8	23.5	1501	17	US-10-282-122A-9150
9	61.4	23.3	214	17	US-10-424-599-126220
10	61.4	23.3	1485	9	US-09-815-242-6958
11	61.4	23.3	1485	17	US-10-282-122A-22036

C	12	61.4	23.3	1830121	17	US-10-329-670-1	Sequence 1, Appl1
C	13	61.4	23.3	1830121	18	US-10-158-865-1	Sequence 1, Appl1
	14	61	23.2	1782	9	US-09-938-842A-2455	Sequence 2455, Ap
	15	61	23.2	1782	11	US-09-938-842A-2455	Sequence 2455, Ap
	16	61	23.2	2232	17	US-10-425-114-16607	Sequence 16607, A
	17	61	23.2	2249	17	US-10-425-114-20264	Sequence 20264, A
	18	61	23.2	2274	17	US-10-425-114-777	Sequence 777, App
	19	61	23.2	2274	17	US-10-425-114-830	Sequence 830, App
	20	61	23.2	2632	18	US-10-425-115-162357	Sequence 162357, A
	21	59.6	22.7	1494	17	US-10-282-122A-12546	Sequence 12546, A
	22	59.6	22.7	6132	11	US-09-809-665A-7	Sequence 7, Appl1
	23	59.6	22.7	6132	18	US-10-854-299-7	Sequence 7, Appl1
	24	59.4	22.6	1464	17	US-10-369-493-40267	Sequence 40267, A
	25	59	22.4	1731	9	US-09-938-842A-156	Sequence 156, App
	26	59	22.4	1731	11	US-09-938-842A-156	Sequence 156, App
	27	58.2	22.1	1476	11	US-10-282-122A-24529	Sequence 24529, A
	28	58.2	22.1	1521	17	US-10-282-122A-21099	Sequence 21099, A
	29	58.2	22.1	1524	9	US-09-815-242-6547	Sequence 6547, Ap
	30	58.2	22.1	32768	9	US-09-070-927A-128	Sequence 128, App
	31	57.4	21.8	1800	9	US-09-938-842A-1621	Sequence 1621, Ap
	32	57.4	21.8	1800	11	US-09-938-842A-1621	Sequence 1621, Ap
	33	57	21.7	840	18	US-10-425-115-109727	Sequence 109727, A
	34	56.4	21.4	1491	17	US-10-282-122A-31151	Sequence 31151, A
	35	55	20.9	1396	17	US-10-424-599-31276	Sequence 31276, A
	36	55	20.9	2328	17	US-10-425-114-6121	Sequence 6121, Ap
	37	55	20.9	2812	17	US-10-424-599-31279	Sequence 31279, A
	38	54.6	20.8	2319	18	US-10-739-930-5533	Sequence 5533, Ap
C	39	53.4	20.3	319630	17	US-10-398-221-7	Sequence 7, Appl1
	40	53.4	20.3	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
	41	53.2	20.2	972	17	US-10-282-122A-35419	Sequence 35419, A
	42	52	19.8	1320	17	US-10-369-493-25834	Sequence 25834, A
	43	52	19.8	1482	17	US-10-369-493-25835	Sequence 25835, A
	44	52	19.8	1524	17	US-10-282-122A-21509	Sequence 21509, A
	45	51.8	19.7	1530	17	US-10-369-493-26367	Sequence 26367, A

ALIGNMENTS

RESULT 1
US-10-425-114-8171
Sequence 8171, Application US/10425114
Publication No. US2004003488BA1
GENERAL INFORMATION:
APPLICANT: Hu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8171
LENGTH: 1680
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700737284_FLI
US-10-425-114-8171

Query Match
Best Local Similarity 89.4%; Score 235; DB 17; Length 1680;
Matches 238; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 GAAGCATTGGATGTTGCCTCATGCTTCGACAGCAGTGCACGCCAGAGGATGG 60
DB 442 GAAGCATTGGATGTTGCCTCATGCTTCGACAGCAGTGCACGCCAGAGGATGG 501
QY 61 AATGCATTAATTTTGAAGAGCATTGGCTTGTATGCATTTTCCCATAGGCTGACA 120

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Db 502 AATGCAATATATTTGAGAACCCATTGGCTTTGATGACCTTCTCCATAGGCTACA 561.
Qy 121 CAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGATTTGATCTACTAGA 180
Db 562 CAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGATTTGATCTACTAGA 621
Qy 181 AGAATCAGTNAATCCCTNAGCTTAAAGGTTTCAANNANAGTTTGAAGCCACT 240
Db 622 AGGAATCTCATGAAATCTTACAGTTTAAAGTTTCAATCTAGTTTGAAGCCACT 681
Qy 241 TNGAGNNAGNACTNNNNGANA 263
Db 682 TGGAGTCGTACTTATATAGATTA 704
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RESULT 2
US-10-424-599-48573

```
/ Sequence 48573, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 48573
/ LENGTH: 2218
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_14868C.1
US-10-424-599-48573
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Query Match 89.4%; Score 235; DB 17; Length 2218;
Best Local Similarity 90.5%; Pred. No. 1.5e-59;
Matches 238; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy 1 GAAGCACTTTTGATGTTGCGTCATGTCTTGCAAGCAGTCTCAGACCCAGAGGATGG 60
Db 894 GAAGCACTTTTGATGTTGCGTCATGTCTTGCAAGCAGTCTCAGACCCAGAGGATGG 953
Qy 61 AATCGCATATATTTGAGAACCCATTGGCTTTGATGACCTTCTCCATAGGCTGACA 120
Db 954 AATCGCATATATTTGAGAACCCATTGGCTTTGATGACCTTCTCCATAGGCTGACA 1013
Qy 121 CAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGATTTGATCTACTAGA 180
Db 1014 CAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGATTTGATCTACTAGA 1073
Qy 181 AGAATCAGTNAATCCCTNAGCTTAAAGGTTTCAANNANAGTTTGAAGCCACT 240
Db 1074 AGGAATCTCATGAAATCTTACAGTTTAAAGTTTCAATCTAGTTTGAAGCCACT 1133
Qy 241 TNGAGNNAGNACTNNNNGANA 263
Db 1134 TGGAGTCGTACTTATATAGATTA 1156
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RESULT 3
US-09-237-183A-2682

```
/ Sequence 2682, Application US/09237183A
/ Publication No. US20030135870A1
/ GENERAL INFORMATION:
/ APPLICANT: Cheikh, Dane K.
/ APPLICANT: Fisher, Dane K.
/ APPLICANT: Liu, Jingsong
/ TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
```

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/ TITLE OF INVENTION: Sucrose Pathway
/ FILE REFERENCE: 38-21(15089)B
/ CURRENT APPLICATION NUMBER: US/09/237,183A
/ CURRENT FILING DATE: 1999-01-26
/ PRIOR APPLICATION NUMBER: US 60/067,000
/ PRIOR FILING DATE: 1997-11-24
/ NUMBER OF SEQ ID NOS: 2814
/ SEQ ID NO 2682
/ LENGTH: 237
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)...(237)
/ OTHER INFORMATION: unsure at all n locations
US-09-237-183A-2682
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Query Match 81.8%; Score 215.2; DB 10; Length 237;
Best Local Similarity 93.2%; Pred. No. 4e-54;
Matches 221; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy 1 GAAGCACTTTTGATGTTGCGTCATGTCTTGCAAGCAGTCTCAGACCCAGAGGATGG 60
Db 1 GAAGCACTTTTGATGTTGCGTCATGTCTTGCAAGCAGTCTCAGACCCAGAGGATGG 60
Qy 61 AATCGCATATATTTGAGAACCCATTGGCTTTGATGACCTTCTCCATAGGCTGACA 120
Db 61 AATCGCATATATTTGAGAACCCATTGGCTTTGATGACCTTCTCCATAGGCTGACA 120
Qy 121 CAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGATTTGATCTACTAGA 180
Db 121 CAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGATTTGATCTACTAGA 180
Qy 181 AGAATCAGTNAATCCCTNAGCTTAAAGGTTTCAANNANAGTTTGAAGCCACT 237
Db 181 AGGAATCTCATGAAATCTTACAGTTTAAAGGTTTCAANNANAGTTTGAAGCCACT 237
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RESULT 4

```
US-09-237-183A-2684
/ Sequence 2684, Application US/09237183A
/ Publication No. US20030135870A1
/ GENERAL INFORMATION:
/ APPLICANT: Fisher, Dane K.
/ APPLICANT: Liu, Jingsong
/ TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
/ FILE REFERENCE: 38-21(15089)B
/ CURRENT APPLICATION NUMBER: US/09/237,183A
/ CURRENT FILING DATE: 1999-01-26
/ PRIOR APPLICATION NUMBER: US 60/067,000
/ PRIOR FILING DATE: 1997-11-24
/ NUMBER OF SEQ ID NOS: 2814
/ SEQ ID NO 2684
/ LENGTH: 260
/ TYPE: DNA
/ ORGANISM: Glycine max
US-09-237-183A-2684
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Query Match 66.8%; Score 175.8; DB 10; Length 260;
Best Local Similarity 87.0%; Pred. No. 2.6e-42;
Matches 180; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Qy 57 AATGATCGCATATATTTGAGAACCCATTGGCTTTGATGACCTTCTCCATAGGCT 116
Db 2 AATGATCGCATATATTTGAGAACCCATTGGCTTTGATGACCTTCTCCATAGGCT 61
Qy 117 GACACAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGATTTGATCTACT 176
Db 62 GACACAATATCTCTTTCAAACTTTGAGAAAAGCAAAATATATAGATTTGATCTACT 121
Qy 177 AGAAGGAATCAGTNAATCCCTNAGCTTAAAGGTTTCAANNANAGTTTGAAGCC 236
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Db 122 AGGAAGATCTCATGAAATCTTACAGTTTAACTGTTTCAAACTAGTTTGGACC 181

Qy 237 ACCTTNGAGNNAGCTNNNNNANNA 263

Db 182 ACTTTGAGTCTGACTTATATAGATTA 208

RESULT 5

US-10-437-963-65487

Sequence 65487, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 65487

LENGTH: 2218

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_66530C.1

US-10-437-963-65487

Query Match 46.8%; Score 123.2; DB 18; Length 2218;

Best Local Similarity 66.0%; Pred. 4.1e-26;

Matches 167; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1 GAAGCATTGTTGATGTCGTCATGCTTTCGAAAGCAGTCTCAGACCCAGAAAGGATG 60

Db 941 GAGGACCTTCTTGATGTTGACGTGCTAGCTAGCAGAGGCCAACTATGCAAGCTTG 1000

Qy 61 AATCGCATATTTTGAAGACCATTTGGCTTTGATGCACTTTCCCATAGGCTGACA 120

Db 1001 AATAGGATATATGAGAAACCATTTGGCTTCACGTTTCTTCACATCGGCTAACA 1060

Qy 121 CAATATCTTCTTCAAACTTTCAGAAAGCAATATATGAATTGATGATCTACTAGGA 180

Db 1061 CAATACCTGCTGTCAGATTTGAGGAGAGCAGATTTACAGATGATCATCTTTGGGG 1120

Qy 181 AGGAATCNCAGTNAANAATCTTCAGGTTTAAAGGTTTCAANNAGTTTGGAGCCACT 240

Db 1121 AAGGATCTGATGAAATCTCACCGCTTGAAGATTTCTTAATTTGGTGTGACCTTTG 1180

Qy 241 TNGAGNNAGCT 253

Db 1181 TGAAGTCGACCT 1193

RESULT 6

US-10-424-599-3107

Sequence 3107, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J

APPLICANT: Kovalic, David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

US-10-424-599-3107

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 3107

LENGTH: 1577

TYPE: DNA

ORGANISM: Glycine max

FEATURE: NAME/KEY: unsure

LOCATION: (1)..(1577)

OTHER INFORMATION: unsure at all n locations

FEATURE: OTHER INFORMATION: unsure at all n locations

US-10-424-599-3107

Query Match 27.3%; Score 71.8; DB 17; Length 1577;

Best Local Similarity 53.6%; Pred. No. 8.3e-11;

Matches 133; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 6 ACTTTGATGTTGGGTGTCATGCTTGAAGCAGTGTCTCAGACCCAGAAAGGATGATG 65

Db 716 ATTGAGATGTTGGAGATGTTGCTAGTCTTAAGCTTCTTCAAAAGATGATGACAG 775

Qy 66 CATTAATATTGAGAGCCATTGGCTTGATGCACTTCTTCCATAGGCTGACACATA 125

Db 776 GGTATATTGTTGAAAAGCCATTGGTGTGATCTCAGATCATCTAGTGAAGTAAAGAG 835

Qy 126 TCTTCTTCAACTTTCAGAAAGCAATATATGATGATGATGATGATGATGATGAT 185

Db 836 TTTGAAGCAGTCTCCTCAGTCAAGACCAATATATGATGATGATGATGATGATGAT 895

Qy 186 TNCAGTNAANAATCTTCAGGTTTAAAGGTTTCAANNAGTTTGGAGCCACTTNGAG 245

Db 896 GCTTGTGAGATATATATGATGATGATGATGATGATGATGATGATGATGATGATG 955

Qy 246 NNGNAGCT 253

Db 956 CCGAATTT 963

RESULT 7

US-10-282-122A-9984

Sequence 9984, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Foreyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9984
;; LENGTH: 1482
;; TYPE: DNA
;; ORGANISM: Bacillus anthracis
US-10-282-122A-9984

Query Match 24.4%; Score 64.2; DB 17; Length 1482;
Best Local Similarity 54.7%; Pred. No. 1.5e-08;
Matches 117; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 31 GCAAGCAGTGTCTGACCCGGAAGGATGGAATCGCATATTTTGAGAAAGCCATTGGC 90
DB 400 GAAAGCGGACTGTGTAAGGATGATGAAAGCGCTAATGATGAAACCGTTGGG 459
QY 91 TTGTATGACCTTTCTTCCATAGGCTGACACAATATCTTCAACTTTGAGAAAG 150
DB 460 CAGGACCTTACATCTGCTCGTAGCTGAATGATAGCTTAGTGCACGTTTGAAAGAC 519
QY 151 CAAATATATGAAATGTGNCATCTACTAGGAAGATCNCAGTAAATCCTTCAGGTTTA 210
DB 520 GAGATATACCGGTATGTATCTATTATTAGGTAGCCGATGATCAAAACCTTGAAAGACCTA 579
QY 211 AGGCTTCAANNAGTTTGTAGCCACCTTNGA 244
DB 580 GAGTTTGCAAAATCCTGTTTACAAATGATTGGA 613

RESULT 8

US-10-282-122A-9150
; Sequence 9150, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931

;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9150
;; LENGTH: 1501
;; TYPE: DNA
;; ORGANISM: Bacillus anthracis
US-10-282-122A-9150

Query Match 23.5%; Score 61.8; DB 17; Length 1501;
Best Local Similarity 55.7%; Pred. No. 8e-08;
Matches 108; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 51 GAAGGATGGAATCGCATATATTGAGAGCCATTGTGCTTGTGATGCACTTCTTCCA 110
DB 414 GATGGATGGAAGCGCTAATGATTGAGAAACGTTGGGACACACCTTACATCTGCTG 473
QY 111 TAGGCTGACACATATCTTCTTCAACTTCAGGAAAGCAATATATAGATTGANCA 170
DB 474 TGAGCTGATGATAGCTTAGCTGACCGTTGAAAGACAGATATACCGTATTGATCA 533
QY 171 TCTACTAGGAAGATCNCAGTAAATCCTNCAGGTTTAGGTTTCAANNAGTTT 230
DB 534 TTATTATAGTAAAGCGATGATTCAAACCTTGAAAGCAGTATGTTGCAATCCTGTTT 593
QY 231 TGAGCCACCTTNGA 244
DB 594 ACCATGATTTGGA 607

RESULT 9

US-10-424-599-126220
; Sequence 126220, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 126220
; LENGTH: 214
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(214)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_84985C.1
US-10-424-599-126220

Query Match 23.3%; Score 61.4; DB 17; Length 214;
Best Local Similarity 67.3%; Pred. No. 4e-08;
Matches 68; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 163 ATTGANCATCTACTAGGAAGATCNCAGTAAATCCTNCAGGTTTAAAGGTTTCAAN 222
DB 1 ATGATCATCTACTAGGAAGATCNCAGTAAATCCTNCAGGTTTAAAGGTTTCAAN 60
QY 223 NNAAGTTTGGACCACTTNGAGNAGNACNTNNNNNANNA 263
DB 61 TTATTTTGGACCATGAAATCCTTACTATGATGATAA 101

RESULT 10

US-09-815-242-6958

; Sequence 6958, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6958

; LENGTH: 1485

; TYPE: DNA

; ORGANISM: Haemophilus influenzae

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1485)

; US-09-815-242-6958

; Query Match 23.3%; Score 61.4; DB 9; Length 1485;

; Best Local Similarity 52.1%; Pred. No. 1e-07;

; Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

; Db 53 AGGATGGAATGCATATATTTGAGAGCCATTGGCTTGATGCACTTTCTCCATA 112

; Db 422 ATGGCTGGAAGATATATCGTTGAAAAACCTTTGGTTACGATGAAAAACAGCCCAA 481

; Db 113 GGCTGACAAATATCTTTCAACTTCAGGAAAAAGCAATATATAGATTGANCATC 172

; Db 482 CATTAGACGTACAAATCCACCGTTCTTTGAGAGAACCAAAATTTATCGATGATCAT 541

; Db 173 TACTAGGAAGATCNCAGTNAATAATCTNCAAGTTTAAAGGTTTCAANNAGNTTTG 232

; Db 542 ATTTAGGTAAAGAAACCGTTCAAAACCTGCTGATTTAGCTTTTCAAAATGTTGTTG 601

; Db 233 AGCCACCTTNGAGNNGNACNTNNNNNANNA 263

; Db 602 AACCGCTTGGAAACCGTAATTTCAATTGATTA 632

; Db 602 AACCGCTTGGAAACCGTAATTTCAATTGATTA 632

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; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 22036

; LENGTH: 1485

; TYPE: DNA

; ORGANISM: Haemophilus influenzae

; US-10-282-122A-22036

; Query Match 23.3%; Score 61.4; DB 17; Length 1485;

; Best Local Similarity 52.1%; Pred. No. 1e-07;

; Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

; Db 53 AGGATGGAATGCATATATTTGAGAGCCATTGGCTTGATGCACTTTCTCCATA 112

; Db 422 ATGGCTGGAAGATATATCGTTGAAAAACCTTTGGTTACGATGAAAAACAGCCCAA 481

; Db 113 GGCTGACAAATATCTTTCAACTTCAGGAAAAAGCAATATATAGATTGANCATC 172

; Db 482 CATTAGACGTACAAATCCACCGTTCTTTGAGAGAACCAAAATTTATCGATGATCAT 541

; Db 173 TACTAGGAAGATCNCAGTNAATAATCTNCAAGTTTAAAGGTTTCAANNAGNTTTG 232

; Db 542 ATTTAGGTAAAGAAACCGTTCAAAACCTGCTGATTTAGCTTTTCAAAATGTTGTTG 601

; Db 233 AGCCACCTTNGAGNNGNACNTNNNNNANNA 263

; Db 602 AACCGCTTGGAAACCGTAATTTCAATTGATTA 632

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; RESULT 12

US-10-329-670-1/C

; Sequence 1, Application US/10329670

; Publication No. US20040018503A1

; GENERAL INFORMATION:

; APPLICANT: Fleischmann et al.

; TITLE OF INVENTION: Sequence of the Haemophilus influenzae Rd Genome, Fragm

; FILE REFERENCE: Theroof, and Uses Theroof

; FILE REFERENCE: PB186PI

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CURRENT APPLICATION NUMBER: US/10/329,670
PRIOR FILING DATE: 2002-12-24
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1830121
TYPE: DNA
ORGANISM: Haemophilus influenzae
FEATURE:
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LOCATION: (9921)..(9921)
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NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a, t, g or c
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GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Frag
FILE REFERENCE: PB186P2CID1
CURRENT APPLICATION NUMBER: US/10/158,865
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1830121
TYPE: DNA
ORGANISM: Haemophilus influenzae
FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,c, or g
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NAME/KEY: misc_feature
LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a,t,c, or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (152530)..(152530)

Query Match 23.3%; Score 61.4; DB 18; Length 1830121;
Best Local Similarity 52.1%; Pred. No. 3.6e-06;
Matches 110; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 53 AGGATGGAAATCCATTAATTTTGAAGCAATTGGCTTGAATGACATTTCTCCATA 112
Db 577356 ATGGCTGGAACGTAATATGTTGAAACCTTTGGTTACATGAAAAACAGCCAAA 577297
QY 113 GGCAGACAAATATCTTCTTCAACCTTCAGGAAGCAAAATATATAGAAATGACATC 172
Db 577296 CATTAAGACGTACAAATCCACCGTTCTTTGAGAACACCAATTTATCGATGATCAT 577237
QY 173 TACTAGGAAGAAATCAAGTAAATCTTCAGGTTTAAAGGTTTCAANNNAAGTTTG 232
Db 577236 ATTTAGTTAAAGAAACCGTTCAAACTTCGTATTTACGTTTCAAAATGGTTGGTTG 577177
QY 233 AGCCACCTTNGAAGNNNAACNTNNNNGANNA 263
Db 577176 AACCGCTTTGGAACGTAATTCATTGATTA 577146
```

RESULT 14

US-09-938-842A-2455

Sequence 2455, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE REFERENCE: SAME, AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/09/938,842A

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 2455

LENGTH: 1782

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-2455

Query Match 23.2%; Score 61; DB 9; Length 1782;
Best Local Similarity 52.1%; Pred. No. 1.5e-07;
Matches 124; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 6 ACTTTGATGTTGGTCAATGCTTGCAGACAGTGTCTGACCCAGAGGAGTGAATCG 65
DB 675 ATTGTAGTGTCTGGAATGTGCAAGCACTTCTGCTCATGTCATGATGAGTACTAG 734
QY 66 CATTAATATTGAGAGCCATTGGCTTTGATGACATTTCTCCCATAGGCTGACACAATA 125
DB 735 GGTATTCGTGCGAAGACCTTTGGTGTGAGATTTCTGAACCTGGCTCTTTAAGCAATC 794
QY 126 TCTTCTTCAAACTTTCAGAAAGCAATATATAGATTGANCATCTACTAGAGAGAA 185
DB 795 CCTCAAGCAGTATTGGAGAGATCAATTTTATAGATAGACATTAAGCAAGAGAA 854
QY 186 TNCAGTNAAAATCCTNCAAGTTTAAGGTTTCAANNAGTTTGAAGCCACCTTNG 243
DB 855 GCTAGTCGAGAACTTATCTGTTCTTCGATTCCAACCTTATATTGAGCCGCTATGG 912

RESULT 15

US-09-938-842A-2455

Sequence 2455, Application US/09938842A

Patent No. US20040009476A9

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE REFERENCE: SAME, AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/09/938,842A

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 2455

LENGTH: 1782

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-2455

Query Match 23.2%; Score 61; DB 11; Length 1782;

Best Local Similarity 52.1%; Pred. No. 1.5e-07;

Matches 124; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 6 ACTTTGATGTTGGTCAATGCTTGCAGACAGTGTCTGACCCAGAGGAGTGAATCG 65
DB 675 ATTGTAGTGTCTGGAATGTGCAAGCACTTCTGCTCATGTCATGATGAGTACTAG 734
QY 66 CATTAATATTGAGAGCCATTGGCTTTGATGACATTTCTCCCATAGGCTGACACAATA 125
DB 735 GGTATTCGTGCGAAGACCTTTGGTGTGAGATTTCTGAACCTGGCTCTTTAAGCAATC 794
QY 126 TCTTCTTCAAACTTTCAGAAAGCAATATATAGATTGANCATCTACTAGAGAGAA 185
DB 795 CCTCAAGCAGTATTGGAGAGATCAATTTTATAGATAGACATTAAGCAAGAGAA 854
QY 186 TNCAGTNAAAATCCTNCAAGTTTAAGGTTTCAANNAGTTTGAAGCCACCTTNG 243
DB 855 GCTAGTCGAGAACTTATCTGTTCTTCGATTCCAACCTTATATTGAGCCGCTATGG 912

Search completed: May 4, 2005, 21:11:33
Job time : 305.387 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 119.974 Seconds

(Without alignments)
5591.830 Million cell updates/sec

Title: US-09-300-482-14

Perfect score: 410

Sequence: 1 cccacgctccgcgcgtcatg.....gcaacgcccgccttgatg 410

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81818359 residues

Total number of hits satisfying chosen parameters: 2405566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*

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5: /cgn2_6/ptodata/1/ina/6C.COMB.seq:*

6: /cgn2_6/ptodata/1/ina/6D.COMB.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186.2	45.4	286	US-09-313-294A-6591	Sequence 6591, Ap
2	161	39.3	277	US-09-313-294A-4756	Sequence 4756, Ap
3	148	36.1	253	US-09-313-294A-6236	Sequence 6236, Ap
4	106.2	25.9	1404	US-09-902-540-4821	Sequence 4821, Ap
5	106.2	25.9	2659	US-09-902-540-1237	Sequence 1237, Ap
6	102	24.9	294	US-09-313-294A-5508	Sequence 5508, Ap
7	99.2	24.2	4403765	US-09-103-840A-2	Sequence 2, Appli
8	89.8	21.9	1830121	US-09-557-884-1	Sequence 1, Appli
9	89.8	21.9	1830121	US-09-643-980A-1	Sequence 1, Appli
10	89.6	21.9	1230025	US-09-198-452A-1	Sequence 1, Appli
11	88	21.5	1230230	US-09-438-185A-1	Sequence 1, Appli
12	85.8	20.9	4411529	US-09-103-840A-1	Sequence 1, Appli
13	75.6	18.4	1471	US-09-543-681A-1179	Sequence 1179, Ap
14	66	16.1	1461	US-09-543-681A-1208	Sequence 1208, Ap
15	62.8	15.3	1407	US-09-710-279-1665	Sequence 1665, Ap
16	62.8	15.3	1425	US-09-134-001C-404	Sequence 404, App
17	62.8	15.3	3516	US-09-710-279-3533	Sequence 3533, Ap
18	62.8	15.3	3773	US-09-710-279-3801	Sequence 3801, Ap
19	56.4	13.8	1953	US-08-961-527-154	Sequence 154, App
20	56.4	13.8	2087	US-09-058-628-1	Sequence 1, Appli
21	56.4	13.8	2087	US-09-584-628-1	Sequence 1, Appli
22	55.2	13.5	411	US-09-513-999C-2113	Sequence 2113, Ap
23	54.6	13.3	1083	US-09-107-433-2083	Sequence 2083, Ap
24	54.6	13.3	1374	US-09-583-110-1306	Sequence 1306, Ap
25	53.4	13.0	777	US-09-248-796A-3106	Sequence 3106, Ap
26	51.2	12.5	578	US-09-621-976-2547	Sequence 2547, Ap
27	49.6	12.1	16592	US-08-956-171E-53	Sequence 53, Appli

C	28	49.6	12.1	16592	4	US-08-781-986A-53	Sequence 53, Appli
	29	46.8	11.4	640681	4	US-09-790-998-1	Sequence 1, Appli
	30	45.4	11.1	960	4	US-09-107-532A-1888	Sequence 1888, Ap
	31	43.2	10.5	972	4	US-09-902-540-8031	Sequence 8031, Ap
	32	43.2	10.5	6715	4	US-09-902-540-818	Sequence 818, App
	33	41.8	10.2	2337	4	US-09-252-991A-2034	Sequence 2034, Ap
	34	41.8	10.2	2475	4	US-09-252-991A-1924	Sequence 1924, Ap
	35	40.4	9.9	2485	4	US-09-252-991A-9419	Sequence 9419, Ap
	36	40.4	9.9	1026	4	US-09-252-991A-9450	Sequence 9450, Ap
	37	40.4	9.9	3417	4	US-09-252-991A-9381	Sequence 9381, Ap
	38	39.6	9.7	16448	4	US-09-902-540-9686	Sequence 9686, Ap
	39	39.6	9.7	16450	4	US-09-902-540-1098	Sequence 1098, Ap
	40	38.4	9.4	24791	4	US-09-902-540-1211	Sequence 1211, Ap
	41	38.2	9.3	969	4	US-09-902-540-2844	Sequence 2844, Ap
	42	38.2	9.3	16047	4	US-09-902-540-1136	Sequence 1136, Ap
	43	37.6	9.3	2363	4	US-09-818-780-22	Sequence 1136, Ap
	44	37.6	9.2	1215	4	US-09-902-540-2767	Sequence 2767, Ap
	45	37.6	9.2	14570	4	US-09-902-540-1012	Sequence 1012, Ap

ALIGNMENTS

RESULT 1

US-09-313-294A-6591

Sequence 6591, Application US/09313294A

Patent No. 6476212

GENERAL INFORMATION:

APPLICANT: Lalagudi, Raghunath V.

APPLICANT: Ito, Laura Y.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR

FILE REFERENCE: PI-0017 US

CURRENT APPLICATION NUMBER: US/09/313, 294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program

SEQ ID NO 6591

LENGTH: 286

TYPE: DNA

ORGANISM: Zea mays

FEATURES:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6476212 700352064H1

NAME/KEY: unsure

LOCATION: 191-192, 194, 233, 255, 264, 276, 281

OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-6591

Query Match

Best Local Similarity

Matches 231; Conservative

45.4%; Score 186.2; DB 4; Length 286;

83.4%; Pred. No. 1.9e-41;

Mismatches 44; Indels 2; Gaps 2;

60

1

120

61

180

121

240

181

229

241

Db

Qy

Db

Qy

Db

Qy

Db

Qy

RESULT 2

US-09-313-294A-4756
; Sequence 4756, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Ito, Laura Y.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; NUMBER OF SEQ ID NOS: 1999-05-14
; SOFTWARE: PERL Program
; SEQ ID NO 4756
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700348987H1
; NAME/KEY: unsure
; LOCATION: 2, 72, 88
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4756

Query Match 39.3%; Score 161; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1,4e-34;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGGTATGGGCGAAGCACTTGCCCTCAACATTGACAGAAAGGTTCCCATCTCTGTG 71
DB 106 GCGGTATGGGCGAAGCACTTGCCCTCAACATTGACAGAAAGGTTCCCATCTCTGTG 165
QY 72 TACACAGACAACTCCCAAGGTGACGAGACCGTGCACCGTCCAGGACAGAAAC 131
DB 166 TACACAGACAACTCCCAAGGTGACGAGACCGTGCACCGTCCAGGACAGAAAC 225
QY 132 CTTCCTGCTACGGCTTCCATGACCCCGGCTCTTTGTGAA 172
DB 226 CTTCCTGCTACGGCTTCCATGACCCCGGCTCTTTGTGAA 266

RESULT 3

US-09-313-294A-6236
; Sequence 6236, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalagudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; NUMBER OF SEQ ID NOS: 1999-05-14
; SOFTWARE: PERL Program
; SEQ ID NO 6236
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351460H1
US-09-313-294A-6236

Query Match 36.1%; Score 148; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 4,9e-31;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGGTATGGGCGAAGCACTTGCCCTCAACATTGACAGAAAGGTTCCCATCTCTGTG 71
DB 106 GCGGTATGGGCGAAGCACTTGCCCTCAACATTGACAGAAAGGTTCCCATCTCTGTG 165

DB 106 GCGGTATGGGCGAAGCACTTGCCCTCAACATTGACAGAAAGGTTCCCATCTCTGTG 165

QY 72 TACACAGACAACTCCCAAGGTGACGAGACCGTGCACCGTCCAGGACAGAAAC 131
DB 166 TACACAGACAACTCCCAAGGTGACGAGACCGTGCACCGTCCAGGACAGAAAC 225

QY 132 CTTCCTGCTACGGCTTCCATGACCCCG 159
DB 226 CTTCCTGCTACGGCTTCCATGACCCCG 253

RESULT 4

US-09-902-540-4821
; Sequence 4821, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4821
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4821

Query Match 25.9%; Score 106.2; DB 4; Length 1404;
Best Local Similarity 56.3%; Pred. No. 2,3e-19;

Matches 223; Conservative 0; Mismatches 164; Indels 9; Gaps 1;

QY 15 GTCATGGGCGAAGCACTTGCCCTCAACATTGACAGAAAGGTTCCCATCTCTGTG 74
DB 25 GTCATGGGCGAAGCACTTGCCCTCAACATTGACAGAAAGGTTCCCATCTCTGTG 84
QY 75 AACAGACAACTCCCAAGGTGACGAGACCGTGCACCGTCCAGGACAGAAACCTT 134
DB 85 AACAGACAACTCCCAAGGTGACGAGACCGTGCACCGTCCAGGACAGAAACCTT 135
QY 135 CCGGTCTACGGCTTCCATGACCCCGGCTCTTTGTGAAAGTCCATTGAGAACCGG 194
DB 136 GAGGTCTGGGCGACCAAGTCTGAGAGCCCTTCTTCAAGCACTGAGAGCGCCCG 195
QY 195 GTGATCATGCTGTCAGAGCGCGCGCGCAATTGACCAACCATGCGACGCTCGAGCT 254
DB 196 GTGCTGTATGTTGACGCGCGCGCGCGCGGAGTCTGATCTGAGAGCGCTGTCGCG 255
QY 255 CACTTGAGAGGCGGACATGATCATGATGAGGAGGAGAGTGTGTAAGAAACAGGAG 314
DB 256 CTGATGCGGAGAGGCGGACATGATGATGAGAGGAGGAGGAGTGTGTAAGAAACAGGAG 315
QY 315 AGGAGGAGAGGCGGACATGATGATGAGAGGAGGAGGAGTGTGTAAGAAACAGGAG 374
DB 316 GCGCGGAGAGGAGTGTGAGAGGAGGAGGAGGAGGAGTGTGTAAGAAACAGGAG 375
QY 375 GGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410
DB 376 GCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 411

RESULT 5

US-09-902-540-1237
; Sequence 1237, Application US/09902540
; Patent No. 6833447

QY 15 GTCATGGGCGAAGCACTTGCCCTCAACATTGACAGAAAGGTTCCCATCTCTGTG 71
DB 25 GTCATGGGCGAAGCACTTGCCCTCAACATTGACAGAAAGGTTCCCATCTCTGTG 84

APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1237
LENGTH: 26659
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-1237

Query Match 25.9%; Score 106.2; DB 4; Length 26659;
Best Local Similarity 56.3%; Pred. No. 6.5e-19;
Matches 223; Conservative 0; Mismatches 164; Indels 9; Gaps 1;

QY 15 GTCAATGGGCGAAGCCTTGCCCTCAACATTGCAAGAAAGGTTCCCATCTCTGTAC 74
DB 10955 GTCAATGGGCGGAGCCTTGCCCTCAACATTGCGAGCAAGGCTTCCGGGTGGCGCTGTGG 11014
QY 75 AACAGACAACCTCCAGAGTGAGAGACCGTGACGCTGCCAAGGCGAAGAAACCTT 134
DB 11015 GACAGGC-----ATCGGAGCGCATTCATGATGATGACCGCAACACGACACCC 11065
QY 135 CCCGCTACGCGCTTCATGACCCCGCTCTTGTGAAGTCCATTGACAGCCAGCGGTG 194
DB 11066 GAGGCTCGGGCCACGAGTCCGTGAGGCTTCGTTGACGCGATGAGACGCGCGCGAAG 11125
QY 195 GTGATCATGCTCTGTCAGAGCGCGCGCAAGTTGACCAAGACCATGCGACGCTCGCACT 254
DB 11126 GTGCTGCTGATGATGATGACGCGCGCGCGGTGAGCTCATGCTGAGACCGCTGTGCG 11185
QY 255 CACTTGAGAGCGGCGCATGATCATGATGAGGAGAAAGAGTGTAGAGAAACGAG 314
DB 11186 CTGATGCGGAGAGGAGCATGATGATGAGACCGCGCAACTCGTGTCTTGACACGCGC 11245
QY 315 AGAGAGGAGAAAGCGCATGAGAGAGCGCGCTTCTGTATCTTGTGAGGTGTCTGTGA 374
DB 11246 CGCGCGGAGAGGAGCATGAGAGGCGCAAGGCAATCCATCTCGGGGCTGCGGTCCGCG 11305
QY 375 GGAAGAGAGGCTGCCCGCAAGCGCGCTCTTGATG 410
DB 11306 GCGAGAGAGGCGCGCGCAAGCGCGCTCTCATGATG 11341

RESULT 6
US-09-313-294A-5508
Sequence 5508, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalugudi, Raghunath V.
APPLICANT: Ito, Laura Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: P1-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 5508
LENGTH: 294
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700350270H1
NAME/KEY: 51
LOCATION: 51
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5508

Query Match 24.9%; Score 102; DB 4; Length 294;
Best Local Similarity 88.4%; Pred. No. 1.9e-18;
Matches 122; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 11 CGCGGTATGGGAGAGACCTTGCCCTCAACATTGCAAGAAAGGTTCCCATCTCTGT 70
DB 158 CGCGGTATGGGAGAGACCTTGCCCTCAACATTGCGGAGAAAGGTTCCCATCTCTGT 217
QY 71 GTACAACAGAGCAACCTTCAAGGTGACGAGACCGTGACGCTGCCAAGGAGAGAA 130
DB 218 CTACAACAGAGCAAC-CTTCAAGGTGATGAGACCGTGACGCTGCCAAGGAGAGAA 276
QY 131 CCTTCCGCTTACGCTT 148
DB 277 CCTCCAGTGTGTGTTT 294

RESULT 7
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 24.2%; Score 99.2; DB 3; Length 4403765;
Best Local Similarity 54.9%; Pred. No. 3.1e-16;
Matches 219; Conservative 0; Mismatches 174; Indels 6; Gaps 1;

QY 12 CGCGTATGGGCGAAGCCTTGCCCTCAACATTGCAAGAAAGGTTCCCATCTCTGT 71
DB 2092322 GCGGTATGGGTTCCCAACATGCGCGAACTTCCCGGACGCTACACGTTGGCAGTG 2092263
QY 72 TACAACAGAGCAACCTTCAAGGTGACGAGACCGTGACGCTGCCAAGGAGAGAAAC 131
DB 2092262 CACAATGCTGTGTCGCCAAGACCGAGCGCTGTTAAGAGCAGAGTCAAGCGGAG 2092203
QY 132 CTTCCTCGTACGCGCTTCATGACCCCGCTCTTGTGAAGTCCATTGACAGCCAGG 191
DB 2092202 T-----TCGTGCGCAGTGAAGATCCCGAATTTCTTGGCGGACATGGAACCCGCGT 2092149
QY 192 GTGTGATCATGCTCTGTCAGAGCGCGGCGCGCAAGTTGACCAAGACATTCGCAAGCTGCA 251
DB 2092148 CGGTGTGATCATGCTCTGTCAGAGCGCGGAGGCGCACTGATCATCAAGAACTTGCT 2092089
QY 252 GCTCACTTGAGAGAGGCGCATGATCATGATGAGGAGGAGAGAGGTTGAGAGAGAGAG 311
DB 2092088 GACGCTATGAAACCGCGGACATATCATGACGCGGCAATGCTGTACACGACACC 2092029
QY 312 GAGAGAGAGAGAGAGCGCATGAGAGAGCGCGCTTCTGTATCTTGTGAGAGGAGGTTCTT 371
DB 2092028 ATGCGCGCGAGAGAGCATGAGAGGCGGCGCTTGTGACCTTGTGCGGCGCGGATCTCC 2091969
QY 372 GAGAGAGAGAGAGGTTGCCCGCAAGCGCGCTCTTGATG 410


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LOCATION: (540001)..(555000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (555001)..(570000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (570001)..(585000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (750001)..(765000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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Query Match
Best Local Similarity 21.9%; Score 89.6; DB 4; Length 1230025;
Matches 213; Conservative 0; Mismatches 180; Indels 6; Gaps 1;
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QY 12 GCGGTGATGGGAGAACCTTGCCCTCAACATTCGAGAGAAAGGTTCCCATCTCTG 71
DB 415812 GCTGTGATGGGAGAAATCTGTCTTAACATGATGATGTTTCTGTCTCTTC 415753
QY 72 TACAACAGACAACTCCAGGTGACAGAACCGTGACGCTGCCAGCAGAGAAAC 131
DB 415752 TATATCGACCCCGAGAGAAACCGGGACCTTGAAGAATACCTTAACACCGAG 415693
QY 132 CTTCCGCTACGAGCTTCATGACCCCGCTCTTTGAGTGCATTCACAAACCGAG 191
DB 415692 CTTGTAAGGTTTGATCTTTGA-----AGACTTTGAAATTCATTGAGAGACGAG 415639
QY 192 GTGTGATCATGCTGTCAGAGCCGCGCCAGTTGACAGACCATGCGACGCTGCA 251
DB 415638 AAGATCATGTGATGATTAAGACAGGAAACCTGTGATCAGACATTCATGCTTACTG 415579
QY 252 GGTCACTTGAGACAGGCGGACTGCATCATGATGGGGAAACGAGTGTGACAGAACG 311
DB 415578 CTTTCTAGAACCCCGGAGATGATATCATGATGGGGAAATGCTATTTAAAGATTCC 415519
QY 312 GAGAGAGAGAGAGAGCCATGAGAGGCGGCGCTTGTATCTTGGCATGGGCTCT 371
DB 415518 GAGAGAGATGTAAGATTAAGATTCCAGAGAAAGGGATTTCTTCTTAGCGTGGGATTTCT 415459
QY 372 GAGAGAAAGAGGGTGCCCGCAACGCGCCGCTTGTATG 410
DB 415458 GAGAGAGAAAGAGGTGACATGACGCGCCATCAATTATG 415420
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RESULT 11

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US-09-438-185A-1/c
Sequence 1, Application US/09438185A
Patent No. 6822071
GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kaiman, Sue
APPLICANT: Davis, Ronald
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1230230
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-438-185A-1
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Query Match
Best Local Similarity 21.5%; Score 88; DB 4; Length 1230230;
Matches 212; Conservative 0; Mismatches 181; Indels 6; Gaps 1;
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QY 12 GCGGTGATGGGAGAACCTTGCCCTCAACATTCGAGAGAAAGGTTCCCATCTCTG 71
DB 405328 GCTGTGATGGGAGAAATCTGTCTTAACATGATGATGTTTCTGTCTCTTC 405269
QY 72 TACAACAGACAACTCCAGGTGACAGAACCGTGACGCTGCCAAGCAGAGAAAC 131
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Db 405268 TATAATCGAACCACAGAAAAAGCGGGAATTCTTGAAGAAATACCTTAACCAACCGAGAG 405209
 Oy 132 CTTCCTCCCTCTACGGCTTCCATGACCCCGGCTCTTTGGAATCCATTGACAGCCAGG 191
 Db 405208 CTGTAGGGGTTTGAATCTTTAGA-----AGATTTTGTGAATTCATTGAGAGACACAGA 405155
 Oy 192 GTGGGATCATGCTGCTCAAGGCGGCGCGGAGTTGACCAAGACATGCGGAGCTCGCA 251
 Db 405154 AAGATCATGTTGATATTCACAGAGAAACCTGTGATCAAGCATTCATGCTTACTG 405095
 Oy 252 GCTCATTTGAGACAGGCGGACTGATCATTCATGCGGGGAAAGAGTGTACAGAAACAG 311
 Db 405094 CTTTTCAGAACCCGCGGATGTGATTCATGAGGGGAAAGATTTTAAAGATTCC 405035
 Oy 312 GAGAGAGGAGAAAGCCATGAGAGAGCGCGCTTCTGTATCTTGGCATGCGGTCTCT 371
 Db 405034 GAACGACCATGTAAAGATTTGAGAAAGAGGAGATTTCTTTTGAAGCGGAGATTCT 404975
 Oy 372 GGAGAAAGAGGAGGCGCGGCAAGCGCGCTTGTATG 410
 Db 404974 GGAGAGAAAGAGGTGACGTCACGCGCCCATCAATTATG 404936

RESULT 12

US-09-103-840A-1/c
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 ; US-09-103-840A-1

Query Match 20.9%; Score 85.8; DB 3; Length 4411529;
 Best Local Similarity 54.2%; Pred. No. 1,4e-12;
 Matches 218; Conservative 0; Mismatches 178; Indels 6; Gaps 2;

Oy 12 GCGGTCATGGGAGCAGAACCTTGCCTCAACATTTGAGAGAAAGGTTCCCATCTCTGTG 71
 Db 2095132 GCCGATGAGGTTCCAAATCGCCGAAACTTCCGCGGACAGGCTACACGCTGACAGT 2095073
 Oy 72 TACAACAGACAACTCCAAAGTGAAGAGACCGTGCACGCTGCCAAGGAGAAAGAAAC 131
 Db 2095072 CACATTCGTCGTGTGCGCAAGCCGACGCTGTAAAGAGCAACAGCTCAACACGCAAG 2095013
 Oy 132 CTTCCTCCCTACAGGCTTCCATGACCCCGGCTCTTTGTGAAGTTCATTCAGAAAGCAAG 191
 Db 2095012 TT---CGTCCGACAGTGAACATATCCCGAATTTCTTCCGACCTGAAAAACCGGCTCG 2094956
 Oy 192 GTGTGATCATGCTC---GTCAAGCGCGCGGCGCAAGTTGACCAAGCAATGCGACGCTC 248
 Db 2094955 GTGTGATCATGCTCAAGCGCGGAGAGGCACTGACGCTGTGATCAACAACTT 2094896
 Oy 249 GCAGCTCATTTGAGAGAGGCGCACTGATCATTCATGAGGGGAGAAAGAGTGTACAGAAC 308
 Db 2094895 GCTGACGCTATGGAACCGCGCAATCATTCATGACGCGGGAAGTGTGACACCGAC 2094836
 Oy 309 ACGGAGAGAGAGAGGCGCAATGAGAGAGCGGCGCTTCTATCTTGGCATGAGGTGTC 368
 Db 2094835 ACCATGCGCGCGAGAAAGCATGCTGAGCGGCGCTTGCATTTGTCGCGGCGCGGATC 2094776

Oy 369 TCTGAGAAAGAGAGGTTCCCGCAAGCGCCGCTCTTGATG 410
 Db 2094775 TCCGCGCGAGAGGCGCGCTTGAACGCGCGCTGATCATG 2094734

RESULT 13

US-09-489-039A-1179
 ; Sequence 1179, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 1179
 ; LENGTH: 1473
 ; TYPE: DNA
 ; ORGANISM: Klebsiella pneumoniae
 ; US-09-489-039A-1179

Query Match 18.4%; Score 75.6; DB 4; Length 1473;
 Best Local Similarity 51.4%; Pred. No. 5.5e-11;
 Matches 205; Conservative 0; Mismatches 185; Indels 9; Gaps 1;

Oy 12 GCGGTCATGGGAGCAGAACCTTGCCTCAACATTTGAGAGAAAGGTTCCCATCTCTGTG 71
 Db 100 GCTGATGAGGCGCTTACCTTGCCTTAACATGAAAGCGGTGTATACGCTTCCTG 159
 Oy 72 TACAACAGACAACTCCAAAGTGAAGAGACCGTGCACGCTGCCAAGGAGAAAGAAAC 131
 Db 160 TTCAACCGCTCCCGGAAAGACGAGAAAGTATGAGAGAAACCCAGGAGAAACTG 219
 Oy 132 CTTCCTCCCTACAGGCTTCCATGACCCCGGCTCTTTGTGAAGTTCATTCAGAAAGCAAG 191
 Db 220 GTTCTTATTAACAGTACAG 270
 Oy 192 GTGTGATCATGCTGTCAAGGCGCGCGCGGCGGAGTGAACCAAGCAATGCGGAGCTGCGA 251
 Db 271 CGTATCTGTGATGAGTGAAGCGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 330
 Oy 252 GCTCATTTGAGAGAGGCGGAGCTGATCATTCATGAGGGGAGAAAGAGTGTGACAGAAACAG 311
 Db 331 CTTTACCTTGAATTAAGGAGCAATCATTCATTTAGGCGGCAACACTTTTCCAGAGACT 390
 Oy 391 ATTCGTGAACCGTGAAGCTGTGTCGCAAGGTTTAACTTATGATGATACGAGTGTTC 450
 Oy 372 GGAGAAAGAGAGGTTCCCGCAAGCGCGCTTCTGATG 410
 Db 451 GGTGTGAAGAGGCGCTGTGAAGGCGCTTCCATCATG 489

RESULT 14

US-09-543-681A-1208
 ; Sequence 1208, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 1208
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1208

Query Match 16.1%; Score 66; DB 4; Length 1461;
Best Local Similarity 49.9%; Pred. No. 2.3e-08;
Matches 199; Conservative 0; Mismatches 191; Indels 9; Gaps 1;

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OY 12 GCGGTCATGGGCGAAGACCTTGGCCCTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 71
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OY 72 TCAACAGAGCAACCTCCAAAGTGCACGACCGTGCAGCGTCCCAAGCAGAGGAAC 131
Db 148 TCAACAGCGCTCGAGCATTAACCAATGAAGTATGCTGAATAATCCAGTAAAAAATCG 207
OY 132 CTTCCTGCTACGCGCTTCCATGACCCCGGCTCTTGTGTAAGTCCATTGAGAACCGG 191
Db 208 GTTCCGAATTACTCTATTGAGA-----ATTGTGATTTCATTAGAAAAACCGCT 258
OY 192 GTGGTATATGCTGCTCAAGCGCGCGCGCAATTGACCAACATCGCGAAGCTCGCA 251
Db 259 CGTATTTTGTATGTTAAAGCGGCTGAAGCAACAGTAAACATCGCAGCCCTGACA 318
OY 252 GCTCACTTGAGAGCGGCGCATCGATCGATGGGGGGAACAGTGTACGAGAACAG 311
Db 319 CCACATTGATTAAGGCGCATCTTATTGATGGCGGAATACTTTCTTTAAAGATACT 378
OY 312 GAGAGAGGAGAGGCGCATGAGAGCGCGCTNCTGTATCTTGATGGCATGGGTCTCT 371
Db 379 ATTCGTCGTAATCGTAGCTATCGGCTCAAGGTTTAACTTATTGTTAGCGGTCTTCT 438
OY 372 GAGAGAAAGAGGGTCCCGCAAGCGCCGCTCTTGATG 410
Db 439 GGTGTGAAGAGGCGCATTTAAAGAACCTTCTATTATG 477
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RESULT 15

US-09-710-279-1665
; Sequence 1665; Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P0348005
; CURRENT APPLICATION NUMBER: US/09/710,279
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1665
; LENGTH: 1407
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-1665

Query Match 15.3%; Score 62.8; DB 4; Length 1407;
Best Local Similarity 49.4%; Pred. No. 1.7e-07;
Matches 197; Conservative 0; Mismatches 193; Indels 9; Gaps 1;

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OY 72 TACAACAGAGCAACCTCCAGAGTGAGACGCGTGCAGCGTCCCAAGGAGAGGAAC 131
Db 91 TATAACGATATCAAGCAAAAAAATGATGATAATGTTAAAGATCGCTTGAAGAGAAATT 150
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OY 132 CTTCCTGCTACGCGTCCATGACCCCGCGCTCTTGTGAAGTCATTCAAGGACGCG 191
Db 151 TACCAACATCTACTATTGAGA-----ATTGTGATCTTTAGAGAACTCTGT 201
OY 192 GTGGTATCATGCTGCTCAAGGCGCGCGCGCAAGTTGACAGACCATGCGAGCTCGCA 251
Db 202 AAGATTTTATTAATGTTAAAGCTGACCTGCACAGATGCCACTATATGATGTTATTA 261
OY 252 GCTCACTTGAGACAGGCGAATGATCATCGATGGGGGGAACGAGTGTACGAGAACAG 311
Db 262 CTTTATTAGAGATGATGATATTTTATTGATGTTAATCTAATTACCAAGATACG 321
OY 312 GAGAGAGGAGAAAGCGCATGAGAGGCGCGCTNCTGTATCTTGATGGCATGGGTCTCT 371
Db 322 ATTCGTCGAAATTAAGCTTGTAGCTGAAGTATTAATTTATTTGTTATGTTAGGATTTCT 381
OY 372 GAGAGAAAGAGGGTCCCGCAAGCGCCGCTCTTGATG 410
Db 382 GGTGAGAAATCGGCGCATCAAGCGGCTTCTTTAATG 420
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 465.167 Seconds
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5365.716 Million cell updates/sec

Title: US-09-300-482-14

Perfect score: 410

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:*

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	396.4	96.7	748	18	US-10-425-115-91003 Sequence 91003, A
2	396.4	96.7	1587	17	US-10-425-114-6537 Sequence 6537, Ap
3	396.4	96.7	1624	17	US-10-425-114-30841 Sequence 30841, A
4	396.4	96.7	1661	17	US-10-425-114-24375 Sequence 24375, A
5	396.4	96.7	1669	17	US-10-425-114-31534 Sequence 31534, A
6	396.4	96.7	1671	17	US-10-425-114-1523 Sequence 1523, Ap
7	396.4	96.7	1672	17	US-10-425-114-24039 Sequence 24039, A
8	396.4	96.7	1672	17	US-10-425-114-32227 Sequence 32227, A
9	396.4	96.7	1674	17	US-10-425-114-13683 Sequence 13683, A
10	396.4	96.7	1675	17	US-10-425-114-446 Sequence 446, Ap
11	396.4	96.7	1691	17	US-10-425-114-28011 Sequence 28011, A

12	396.4	96.7	1781	17	US-10-425-114-3294 Sequence 3294, Ap
13	396.4	96.7	1798	17	US-10-425-114-508 Sequence 508, Ap
14	396.4	96.7	3520	18	US-10-425-115-91000 Sequence 91000, Ap
15	396.4	96.3	2171	17	US-10-425-114-2633 Sequence 2633, Ap
16	394.8	96.3	2469	18	US-10-425-115-91002 Sequence 91002, A
17	393.2	95.9	1650	17	US-10-425-114-3149 Sequence 3149, Ap
18	393.2	95.9	1678	17	US-10-425-114-4238 Sequence 4238, Ap
19	393.2	95.9	1678	17	US-10-425-114-13538 Sequence 13538, A
20	393.2	95.9	1678	17	US-10-425-114-24256 Sequence 24256, A
21	393.2	95.9	1681	17	US-10-425-114-25038 Sequence 25038, A
22	393.2	95.9	1681	17	US-10-425-114-4096 Sequence 4096, Ap
23	393.2	95.9	1684	17	US-10-425-114-25153 Sequence 25153, A
24	393.2	95.9	1686	17	US-10-425-114-3615 Sequence 3615, Ap
25	393.2	95.9	1728	17	US-10-425-114-4434 Sequence 4434, Ap
26	393.2	95.9	1740	17	US-10-425-114-24479 Sequence 24479, A
27	393.2	95.9	1798	17	US-10-425-114-1418 Sequence 1418, Ap
28	391.6	95.5	1872	17	US-10-425-114-26662 Sequence 26662, A
29	360	87.8	637	18	US-10-425-114-12436 Sequence 12436, A
30	360	87.8	637	18	US-10-425-115-91011 Sequence 91011, A
31	346.8	84.6	1953	18	US-10-767-701-14931 Sequence 14931, A
32	326	79.5	1831	18	US-10-437-963-98959 Sequence 98959, A
33	323.8	79.0	1755	17	US-10-425-114-32383 Sequence 32383, A
34	323.8	79.0	1776	17	US-10-425-114-3640 Sequence 3640, Ap
35	323.8	79.0	2343	18	US-10-425-115-127057 Sequence 127057, A
36	322.2	78.6	1125	18	US-10-425-115-44970 Sequence 44920, A
37	302.8	73.9	510	18	US-10-425-115-54519 Sequence 54519, A
38	262	63.9	1785	18	US-10-739-930-1129 Sequence 1129, Ap
39	242.8	59.2	1627	17	US-10-425-114-10641 Sequence 10641, A
40	242.8	59.2	1838	17	US-10-424-599-76904 Sequence 76904, A
41	234.8	57.3	4825	17	US-10-424-599-59918 Sequence 59918, A
42	231.6	56.5	1737	17	US-10-425-114-12849 Sequence 12849, A
43	230	56.1	2691	17	US-10-424-599-59294 Sequence 59294, A
44	215.8	52.6	286	9	US-09-294-093B-5229 Sequence 5229, Ap
45	207.6	50.6	901	17	US-10-424-599-66028 Sequence 66028, A

ALIGNMENTS

RESULT 1
US-10-425-115-91003
; Sequence 91003, Application US/10425115
; Publication No. US2004021472NA1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 91003
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: M8T4577_182998C.1
; US-10-425-115-91003

Query Match 96.7%; Score 396.4; DB 18; Length 748;
Best Local Similarity 99.5%; Pred. No. 2.7e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGCGACAGACCTTGCTCCATTCAGAGAGAAAGGTTCCCATCTCTGTG 71
DB 205 GCGGTCATGGGCGACAGACCTTGCTCCATTCAGAGAGAAAGGTTCCCATCTCTGTG 264
QY 72 TACAACAGAGACCACTCCAGAGGTGAGAGACCGTGACGCGTGCCAGGACAGAGGAAC 131
DB 285 TACAACAGAGACCACTCCAGAGGTGAGAGACCGTGACGCGTGCCAGGACAGAGGAAC 324

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Db 325 CTTCCCGTCTAGGCTTCCATGACCCCGCCCTTTGTGAAGTCCATTGAGAACCCACGG 384
QY 192 GTGTGATCATGCTCGTCAAGCCCGCGCCGAGTTCACGACCATTCGCGAGCTCGCA 251
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Db 385 GTGTGATCATGCTCGTCAAGCCCGCGCCGAGTTCACGACCATTCGCGAGCTCGCA 444
QY 252 GCTCACTTGGAGCGCGCCGAGTTCATGATGATGAGGGGAAACGAGTGTACGAGAACCG 311
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Db 445 GCTCACTTGGAGCGCGCCGAGTTCATGATGATGAGGGGAAACGAGTGTACGAGAACCG 504
QY 312 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 371
|
Db 505 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 564
QY 372 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 410
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Db 565 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 603
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RESULT 2

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US-10-425-114-6537
/ Sequence 6537, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 6537
/ LENGTH: 1587
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700570587_FLI
US-10-425-114-6537
```

Query Match 96.7%; Score 396.4; DB 17; Length 1587;
Best Local Similarity 99.5%; Pred. No. 36-113;

Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 12 GCGGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 71
|
Db 33 GCGGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 92
QY 72 TACAACAGAGCAACCTCCCAAGGTGAGAGACCCGCGCGCTTTGTGAAGTCCATTGAGAAC 131
|
Db 93 TACAACAGAGCAACCTCCCAAGGTGAGAGACCCGCGCGCTTTGTGAAGTCCATTGAGAAC 152
QY 132 CTTCCCGTCTAGGCTTCCATGACCCCGCCCTTTGTGAAGTCCATTGAGAACCCACGG 191
|
Db 153 CTTCCCGTCTAGGCTTCCATGACCCCGCCCTTTGTGAAGTCCATTGAGAACCCACGG 212
QY 192 GTGTGATCATGCTCGTCAAGCCCGCGCCGAGTTCACGACCATTCGCGAGCTCGCA 251
|
Db 213 GTGTGATCATGCTCGTCAAGCCCGCGCCGAGTTCACGACCATTCGCGAGCTCGCA 272
QY 252 GCTCACTTGGAGCGCGCCGAGTTCATGATGATGAGGGGAAACGAGTGTACGAGAACCG 311
|
Db 273 GCTCACTTGGAGCGCGCCGAGTTCATGATGATGAGGGGAAACGAGTGTACGAGAACCG 332
QY 312 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 371
|
```

```
Db 333 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 392
QY 372 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 410
|
Db 393 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 431
```

RESULT 3

```
US-10-425-114-30841
/ Sequence 30841, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 30841
/ LENGTH: 1624
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: UC-ZMFLB73088H07_FLI
US-10-425-114-30841
```

Query Match 96.7%; Score 396.4; DB 17; Length 1624;
Best Local Similarity 99.5%; Pred. No. 36-113;

Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 12 GCGGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 71
|
Db 70 GCGGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 129
QY 72 TACAACAGAGCAACCTCCCAAGGTGAGAGACCCGCGCGCTTTGTGAAGTCCATTGAGAAC 131
|
Db 130 TACAACAGAGCAACCTCCCAAGGTGAGAGACCCGCGCGCTTTGTGAAGTCCATTGAGAAC 189
QY 132 CTTCCCGTCTAGGCTTCCATGACCCCGCCCTTTGTGAAGTCCATTGAGAACCCACGG 191
|
Db 190 CTTCCCGTCTAGGCTTCCATGACCCCGCCCTTTGTGAAGTCCATTGAGAACCCACGG 249
QY 192 GTGTGATCATGCTCGTCAAGCCCGCGCCGAGTTCACGACCATTCGCGAGCTCGCA 251
|
Db 250 GTGTGATCATGCTCGTCAAGCCCGCGCCGAGTTCACGACCATTCGCGAGCTCGCA 309
QY 252 GCTCACTTGGAGCGCGCCGAGTTCATGATGATGAGGGGAAACGAGTGTACGAGAACCG 311
|
Db 310 GCTCACTTGGAGCGCGCCGAGTTCATGATGATGAGGGGAAACGAGTGTACGAGAACCG 369
QY 312 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 371
|
Db 370 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 429
QY 372 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 410
|
Db 430 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 468
```

RESULT 4

```
US-10-425-114-24375
/ Sequence 24375, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
```

APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO: 24375
LENGTH: 1661
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3608-041-E4_FLI
US-10-425-114-24375

Query Match 96.7%; Score 396.4; DB 17; Length 1661;
Best Local Similarity 99.5%; Pred. No. 3e-113; Indels 0; Gaps 0;
Matches 397; Conservative 0; Mismatches 2;

QY 12 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 71
Db 107 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 166

QY 72 TACAACAGAGAACCTCCAGAGTGAAGAGACCGTGCAGCGTCCAGAGAGAGAAAC 131
Db 167 TACAACAGAGAACCTCCAGAGTGAAGAGACCGTGCAGCGTCCAGAGAGAGAAAC 226

QY 132 CTTCCCGCTACAGGCTTCCATGACCCCGCGTCTTGTGAAGTCCATTGAGAGAGAG 191
Db 227 CTTCCCGCTACAGGCTTCCATGACCCCGCGTCTTGTGAAGTCCATTGAGAGAGAG 286

QY 192 GTGGTATCATGCTCTGTCAGAGCGCGCGGCGGCAAGTTGACAGACCATGCGAGCGTGC 251
Db 287 GTGGTATCATGCTCTGTCAGAGCGCGCGGCGGCAAGTTGACAGACCATGCGAGCGTGC 346

QY 252 GCTCACTTGGAGAGAGGCGAGCTGATCATGAGGGGGAGAGAGTGTAGAGAGACAG 311
Db 347 GCTCACTTGGAGAGAGGCGAGCTGATCATGAGGGGGAGAGAGTGTAGAGAGACAG 406

QY 312 GAGAGAGAGAGAGAGGCGATGAGAGAGCGCGGCTNCTGTATCTTGGAGATGGGTCTCT 371
Db 407 GAGAGAGAGAGAGAGGCGATGAGAGAGCGCGGCTNCTGTATCTTGGAGATGGGTCTCT 466

QY 372 GAGAGAGAGAGAGGCTGCGGAGAGAGCGCGGCTGCTTGTATG 410
Db 467 GAGAGAGAGAGAGGCTGCGGAGAGAGCGCGGCTGCTTGTATG 505

RESULT 5
US-10-425-114-31534
Sequence 31534, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO: 31534
LENGTH: 1669
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73186B12_FLI

US-10-425-114-31534

Query Match 96.7%; Score 396.4; DB 17; Length 1669;
Best Local Similarity 99.5%; Pred. No. 3e-113; Indels 0; Gaps 0;
Matches 397; Conservative 0; Mismatches 2;

QY 12 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 71
Db 115 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 174

QY 72 TACAACAGAGAACCTCCAGAGTGAAGAGACCGTGCAGCGTCCAGAGAGAGAAAC 131
Db 175 TACAACAGAGAACCTCCAGAGTGAAGAGACCGTGCAGCGTCCAGAGAGAGAAAC 234

QY 132 CTTCCCGCTACAGGCTTCCATGACCCCGCGTCTTGTGAAGTCCATTGAGAGAGAG 191
Db 235 CTTCCCGCTACAGGCTTCCATGACCCCGCGTCTTGTGAAGTCCATTGAGAGAGAG 294

QY 192 GTGGTATCATGCTCTGTCAGAGCGCGGCGGCGGCAAGTTGACAGACCATGCGAGCGTGC 251
Db 295 GTGGTATCATGCTCTGTCAGAGCGCGGCGGCGGCAAGTTGACAGACCATGCGAGCGTGC 354

QY 252 GCTCACTTGGAGAGAGGCGAGCTGATCATGATGAGGGGGAGAGAGTGTAGAGAGACAG 311
Db 355 GCTCACTTGGAGAGAGGCGAGCTGATCATGATGAGGGGGAGAGAGTGTAGAGAGACAG 414

QY 312 GAGAGAGAGAGAGAGGCGATGAGAGAGCGCGGCTNCTGTATCTTGGAGATGGGTCTCT 371
Db 415 GAGAGAGAGAGAGAGGCGATGAGAGAGCGCGGCTNCTGTATCTTGGAGATGGGTCTCT 474

QY 372 GAGAGAGAGAGAGGCTGCGGAGAGAGCGCGGCTGCTTGTATG 410
Db 475 GAGAGAGAGAGAGGCTGCGGAGAGAGCGCGGCTGCTTGTATG 513

RESULT 6
US-10-425-114-1523
Sequence 1523, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO: 1523
LENGTH: 1671
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700156333_FLI
US-10-425-114-1523

Query Match 96.7%; Score 396.4; DB 17; Length 1671;
Best Local Similarity 99.5%; Pred. No. 3e-113; Indels 0; Gaps 0;
Matches 397; Conservative 0; Mismatches 2;

QY 12 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 71
Db 117 GCGGTCATGGGCGAGAACTTGGCCCTCAACATTGAGAGAAAGGTTCCCATCTCTGTG 176

QY 72 TACAACAGAGAACCTCCAGAGTGAAGAGACCGTGCAGCGTCCAGAGAGAGAAAC 131
Db 177 TACAACAGAGAACCTCCAGAGTGAAGAGACCGTGCAGCGTCCAGAGAGAGAAAC 236

QY 132 CTTCCCGCTACAGGCTTCCATGACCCCGCGTCTTGTGAAGTCCATTGAGAGAGAGAG 191

```
Db      237 CTTCCTGCTACGGTTCATGATACCCCGCGCTCTTGTGAATGTCATTCAAAACCCACGG 296
Qy      192 GTGGTATCATGCTGCTCAAGCGCGCGCCAGTTGACAGACCATCGACGCTCGCA 251
Db      297 GTGGTATCATGCTGCTCAAGCGCGCGCCAGTTGACAGACCATCGACGCTCGCA 356
Qy      252 GCTCACTTGAAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 311
Db      357 GCTCACTTGAAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 416
Qy      312 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 371
Db      417 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 476
Qy      372 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 410
Db      477 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 515
```

RESULT 7

```
US-10-425-114-24039
; Sequence 24039, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 24039
; LENGTH: 1672
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3607-006-H2_FLI
US-10-425-114-24039
```

```
Query Match      96.7%; Score 396.4; DB 17; Length 1672;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      12 GGGGTCATGGGGGAGAACTTGCCTCAACATTGCAAGAGAAAGGTTCCCATCTCTGTG 71
Db      118 GCGGTCAATGGGGGAGAACTTGCCTCAACATTGCAAGAGAAAGGTTCCCATCTCTGTG 177
Qy      72 TACAACAGAGAACCTCCCAAGGTGAGACGACGCGCGCCAGCCCAAGAGGAGAAAC 131
Db      178 TACAACAGAGAACCTCCCAAGGTGAGACGACGCGCGCCAGCCCAAGAGGAGAAAC 237
Qy      132 CTTCCTGCTACAGGCTTCCATGACCCCGCTCTTGTGAAGTCCATTCAAGCCACG 191
Db      238 CTTCCTGCTACAGGCTTCCATGACCCCGCTCTTGTGAAGTCCATTCAAGCCACG 297
Qy      192 GTGGTATCATGCTGCTCAAGCGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 311
Db      298 GTGGTATCATGCTGCTCAAGCGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 357
Qy      252 GCTCACTTGAAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 371
Db      358 GCTCACTTGAAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 417
Qy      312 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 371
Db      418 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 477
```

```
Qy      372 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 410
Db      478 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 516
```

RESULT 8

```
US-10-425-114-32227
; Sequence 32227, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32227
; LENGTH: 1672
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73276H04_FLI
US-10-425-114-32227
```

```
Query Match      96.7%; Score 396.4; DB 17; Length 1672;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      12 GCGGTCAATGGGGGAGAACTTGCCTCAACATTGCAAGAGAAAGGTTCCCATCTCTGTG 71
Db      118 GCGGTCAATGGGGGAGAACTTGCCTCAACATTGCAAGAGAAAGGTTCCCATCTCTGTG 177
Qy      72 TACAACAGAGAACCTCCCAAGGTGAGACGACGCGCGCCAGCCCAAGAGGAGAAAC 131
Db      178 TACAACAGAGAACCTCCCAAGGTGAGACGACGCGCGCCAGCCCAAGAGGAGAAAC 237
Qy      132 CTTCCTGCTACAGGCTTCCATGACCCCGCTCTTGTGAAGTCCATTCAAGCCACG 191
Db      238 CTTCCTGCTACAGGCTTCCATGACCCCGCTCTTGTGAAGTCCATTCAAGCCACG 297
Qy      192 GTGGTATCATGCTGCTCAAGCGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 311
Db      298 GTGGTATCATGCTGCTCAAGCGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 357
Qy      252 GCTCACTTGAAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 371
Db      358 GCTCACTTGAAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 417
Qy      312 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 371
Db      418 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 477
Qy      372 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 410
Db      478 GAGAGGAGGAGGAGGCGGAGCTGATCATGATGCGGGAACGAGTGTACGAGAACAGC 516
```

RESULT 9

```
US-10-425-114-13683
; Sequence 13683, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
```


APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 13683
LENGTH: 1674
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB143-023-B9_FLI
US-10-425-114-13683

Query Match 96.7%; Score 396.4; DB 17; Length 1674;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGGCAGAACCTTGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGTG 71
DB 120 GCGGTCATGGGGCAGAACCTTGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGTG 179
QY 72 TACAACAGAGACAACTCCCAAGGTGAGAGAACCGTGACAGCGTCCCAAGGACAGAAAGAAC 131
DB 180 TACAACAGAGACAACTCCCAAGGTGAGAGAACCGTGACAGCGTCCCAAGGACAGAAAGAAC 239
QY 132 CTTCCTGCTACGCGCTTCATGACCGCGCGTCTTTGTGAAGTTCATTCAGAACCGCAG 191
DB 240 CTTCCTGCTACGCGCTTCATGACCGCGCGTCTTTGTGAAGTTCATTCAGAACCGCAG 299
QY 192 GTGGTATCATGCTCTGTCAAGGCGCGCGCGCGTTCAGTTCAGAACCATTCGCGACGCTCGCA 251
DB 300 GTGGTATCATGCTCTGTCAAGGCGCGCGCGCGTTCAGTTCAGAACCATTCGCGACGCTCGCA 359
QY 252 GCTCACTTGAGACAGAGCGCATGTCATTCATTCAGTGGGGGAGAGAGTGTACAGAAACAG 311
DB 360 GCTCACTTGAGACAGAGCGCATGTCATTCATTCAGTGGGGGAGAGAGTGTACAGAAACAG 419
QY 312 GAGAGAGAGAGAGAGCGCATGAGAGAGCGCGCTTCTGTATCTTGAGATGGGTGTCTCT 371
DB 420 GAGAGAGAGAGAGAGCGCATGAGAGAGCGCGCTTCTGTATCTTGAGATGGGTGTCTCT 479
QY 372 GAGAGAGAGAGAGCGTCCCGCAACGCGCGCTCTTGATG 410
DB 480 GAGAGAGAGAGAGCGTCCCGCAACGCGCGCTCTTGATG 518

RESULT 10

US-10-425-114-446
Sequence 446, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 446
LENGTH: 1675
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700075354_FLI
US-10-425-114-446

Query Match 96.7%; Score 396.4; DB 17; Length 1675;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGGCAGAACCTTGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGTG 71
DB 121 GCGGTCATGGGGCAGAACCTTGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGTG 180
QY 72 TACAACAGAGACAACTCCCAAGGTGAGAGAACCGTGACAGCGTCCCAAGGACAGAAAGAAC 131
DB 181 TACAACAGAGACAACTCCCAAGGTGAGAGAACCGTGACAGCGTCCCAAGGACAGAAAGAAC 240
QY 132 CTTCCTGCTACGCGCTTCATGACCGCGCGTCTTTGTGAAGTTCATTCAGAACCGCAG 191
DB 241 CTTCCTGCTACGCGCTTCATGACCGCGCGTCTTTGTGAAGTTCATTCAGAACCGCAG 300
QY 192 GTGGTATCATGCTCTGTCAAGGCGCGCGCGCGTTCAGTTCAGAACCATTCGCGACGCTCGCA 251
DB 301 GTGGTATCATGCTCTGTCAAGGCGCGCGCGCGTTCAGTTCAGAACCATTCGCGACGCTCGCA 360
QY 252 GCTCACTTGAGACAGAGCGCATGTCATTCATTCAGTGGGGGAGAGAGTGTACAGAAACAG 311
DB 361 GCTCACTTGAGACAGAGCGCATGTCATTCATTCAGTGGGGGAGAGAGTGTACAGAAACAG 420
QY 312 GAGAGAGAGAGAGCGCATGAGAGAGCGCGCTTCTGTATCTTGAGATGGGTGTCTCT 371
DB 421 GAGAGAGAGAGAGCGCATGAGAGAGCGCGCTTCTGTATCTTGAGATGGGTGTCTCT 480
QY 372 GAGAGAGAGAGAGCGTCCCGCAACGCGCGCTCTTGATG 410
DB 481 GAGAGAGAGAGAGCGTCCCGCAACGCGCGCTCTTGATG 519

RESULT 11

US-10-425-114-28011
Sequence 28011, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28011
LENGTH: 1691
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4743-047-F5_FLI
US-10-425-114-28011

Query Match 96.7%; Score 396.4; DB 17; Length 1691;
Best Local Similarity 99.5%; Pred. No. 3e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCATGGGGCAGAACCTTGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGTG 71
DB 134 GCGGTCATGGGGCAGAACCTTGCCCTCAACATTCAGAGAAAGGTTCCCATCTCTGTG 193
QY 72 TACAACAGAGACAACTCCCAAGGTGAGAGAACCGTGACAGCGTCCCAAGGACAGAAAGAAC 131
DB 194 TACAACAGAGACAACTCCCAAGGTGAGAGAACCGTGACAGCGTCCCAAGGACAGAAAGAAC 253
QY 132 CTTCCTGCTACGCGCTTCATGACCGCGCGTCTTTGTGAAGTTCATTCAGAACCGCAG 191
DB 254 CTTCCTGCTACGCGCTTCATGACCGCGCGTCTTTGTGAAGTTCATTCAGAACCGCAG 313

;; CURRENT APPLICATION NUMBER: US/10/425,115
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 369326
;; SEQ ID NO 91000
;; LENGTH: 3520
;; TYPE: DNA
;; ORGANISM: Zea mays
;; FEATURE:
;; OTHER INFORMATION: Clone ID: MRT4577_182995C.1
US-10-425-115-91000

Query Match 96.7%; Score 396.4; DB 18; Length 3520;
Best Local Similarity 99.5%; Pred. No. 3.4e-113;
Matches 397; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 GCGGTCAATGAGGAGCAACCTTCCCTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 71
DB 1319 GCGGTCAATGAGGAGCAACCTTCCCTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 1378

QY 72 TACAACAGGACAACTCCCAAGGTGACGACCGTGCAGCGCCAGGCAAGGCAAGAGAAAC 131
DB 1379 TACAACAGGACAACTCCCAAGGTGACGACCGTGCAGCGCCAGGCAAGGCAAGAGAAAC 1438

QY 132 CTTCCCGTCTACGCGCTTCCATGACCCCGCGTCTTTGTGAAGTCCATTGAGACCAACG 191
DB 1439 CTTCCCGTCTACGCGCTTCCATGACCCCGCGTCTTTGTGAAGTCCATTGAGACCAACG 1498

QY 192 GTGTGATCATGCTGTCTCAAGCGCGCGCCGACGTTGACCAACCATGCGACGCTCGCA 251
DB 1499 GTGTGATCATGCTGTCTCAAGCGCGCGCCGACGTTGACCAACCATGCGACGCTCGCA 1558

QY 252 GCTCACTTGAGAGGAGGAGCTGCATTCATTCGATGGGGGGAAGAGTGTGACGAGAAACAG 311
DB 1559 GCTCACTTGAGAGGAGGAGCTGCATTCATTCGATGGGGGGAAGAGTGTGACGAGAAACAG 1618

QY 312 GAGAGGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 371
DB 1619 GAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1678

QY 372 GAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410
DB 1679 GAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1717

RESULT 15
US-10-425-114-2633
;; Sequence 2633, Application US/10425114
;; Publication No. US2004003488A1
;; GENERAL INFORMATION:
;; APPLICANT: Liu, Jingdong
;; APPLICANT: Zhou, Yihua
;; APPLICANT: Kovalic, David K.
;; APPLICANT: Screen, Steven E
;; APPLICANT: Tabaska, Jack E
;; APPLICANT: Cao, Yongwei
;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53313)B
;; CURRENT APPLICATION NUMBER: US/10/425,114
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 73128
;; SEQ ID NO 2633
;; LENGTH: 2171
;; TYPE: DNA
;; ORGANISM: Zea mays
;; FEATURE:
;; OTHER INFORMATION: Clone ID: 700219903_FLI
US-10-425-114-2633

Query Match 96.3%; Score 394.8; DB 17; Length 2171;
Best Local Similarity 99.2%; Pred. No. 1e-112;
Matches 396; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 GCGGTCAATGAGGAGCAACCTTCCCTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 71
DB 617 GCGGTCAATGAGGAGCAACCTTCCCTCAACATTGACAGAGAAAGGTTCCCATCTCTGTG 676

QY 72 TACAACAGGACAACTCCCAAGGTGACGACCGTGCAGCGCCAGGCAAGGCAAGAGAAAC 131
DB 677 TACAACAGGACAACTCCCAAGGTGACGACCGTGCAGCGCCAGGCAAGGCAAGAGAAAC 736

QY 132 CTTCCCGTCTACGCGCTTCCATGACCCCGCGTCTTTGTGAAGTCCATTGAGACCAACG 191
DB 737 CTTCCCGTCTACGCGCTTCCATGACCCCGCGTCTTTGTGAAGTCCATTGAGACCAACG 796

QY 192 GTGTGATCATGCTGTCTCAAGCGCGCGCCAGTTCACAGACCATGCGCGCTCGCA 251
DB 797 GTGTGATCATGCTGTCTCAAGCGCGCGCCAGTTCACAGACCATGCGCGCTCGCA 856

QY 252 GCTCACTTGAGAGGAGGAGCTGCATTCATTCGATGGGGGGAAGAGTGTGACGAGAAACAG 311
DB 857 GCTCACTTGAGAGGAGGAGCTGCATTCATTCGATGGGGGGAAGAGTGTGACGAGAAACAG 916

QY 312 GAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 371
DB 917 GAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 976

QY 372 GAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410
DB 977 GAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1015

Search completed: May 4, 2005, 21:11:35
Job time : 467.167 secs

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RESULT 2
 US-09-134-001C-2798
 ; Sequence 2798, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

/ TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: GTC-007
/ CURRENT APPLICATION NUMBER: US/09/134,001C
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/064,964
/ PRIOR FILING DATE: 1997-11-08
/ PRIOR APPLICATION NUMBER: US 60/055,779
/ PRIOR FILING DATE: 1997-08-14
/ NUMBER OF SEQ ID NOS: 5674
/ SEQ ID NO 2798
/ LENGTH: 507
/ TYPE: DNA
/ ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2798

Query Match 14.8%; Score 34.6; DB 3; Length 507;
Best Local Similarity 61.8%; Pred. No. 0.095;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 11 TTACTAGAAATATGTTAGTGGCTCCTATGATAGGAGGATTTGAGTTATGAAATGAG 70
DB 310 TTAGAAGATTTAATTAATGACCAAGAGATTAATGCGCAATTATTAATGTAATCAA 369

QY 71 GCAATCTCTGAGTATGAGACTTCAGAAA 99
DB 370 CTAACTCTGATTATCAAAACCCAGAGA 398

RESULT 3
US-09-710-279-185
/ Sequence 185, Application US/09/10279
/ Patent No. 6703492
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/09/710,279
/ CURRENT FILING DATE: 2000-11-09
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 185
/ LENGTH: 597
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: nucleic acid sequence
US-09-710-279-185

Query Match 14.8%; Score 34.6; DB 4; Length 597;
Best Local Similarity 61.8%; Pred. No. 0.1;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 11 TTACTAGAAATATGTTAGTGGCTCCTATGATAGGAGGATTTGAGTTATGAAATGAG 70
DB 436 TTAGAAGATTTAATTAATGACCAAGAGTACTGGCAATTATTAATGTAATCAA 495

QY 71 GCAATCTCTGAGTATGAGACTTCAGAAA 99
DB 496 CTAACTCTGATTATCAAAACCCAGAGA 524

RESULT 4
US-09-710-279-3371/c
/ Sequence 3371, Application US/09/10279
/ Patent No. 6703492
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/09/710,279

/ CURRENT FILING DATE: 2000-11-09
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 3371
/ LENGTH: 2945
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3371

Query Match 14.8%; Score 34.6; DB 4; Length 2945;
Best Local Similarity 61.8%; Pred. No. 0.21;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 11 TTACTAGAAATATGTTAGTGGCTCCTATGATAGGAGGATTTGAGTTATGAAATGAG 70
DB 162 TTAGAAGATTTAATTAATGACCAAGAGATTAATGCGCAATTATTAATGTAATCAA 103

QY 71 GCAATCTCTGAGTATGAGACTTCAGAAA 99
DB 102 CTAACTCTGATTATCAAAACCCAGAGA 74

RESULT 5
US-09-710-279-3794/c
/ Sequence 3794, Application US/09/10279
/ Patent No. 6703492
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/09/710,279
/ CURRENT FILING DATE: 2000-11-09
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 3794
/ LENGTH: 3825
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3794

Query Match 14.8%; Score 34.6; DB 4; Length 3825;
Best Local Similarity 61.8%; Pred. No. 0.24;
Matches 55; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 11 TTACTAGAAATATGTTAGTGGCTCCTATGATAGGAGGATTTGAGTTATGAAATGAG 70
DB 780 TTAGAAGATTTAATTAATGACCAAGAGTACTGGCAATTATTAATGTAATCAA 721

QY 71 GCAATCTCTGAGTATGAGACTTCAGAAA 99
DB 720 CTAACTCTGATTATCAAAACCCAGAGA 692

RESULT 6
US-09-949-016-17375/c
/ Sequence 17375, Application US/09/949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: C1001307
/ CURRENT APPLICATION NUMBER: US/09/949,016

```

:      LENGTH: 4358 base pairs
:      TYPE: nucleic acid
:      STRANDEDNESS: double
:      TOPOLOGY: linear
:      US-08-781-986A-454

Query Match      13.4% Score 31.2: DB 4: length 4358:

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Best Local Similarity 53.2%; Pred. No. 3.6;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 48 AAGATTGAGTTGATGATGAGCAATCTCTGATGAGACTTCGAAACATGACT 107
Db 1252 AAAGATTTTGTGTTTATCTGGAATTTTAAAGAAAAACGAGCAGTGAAC 1311
QY 108 CGGAGACTACCGAGATTTATTTTGGCATTCCTCATGCTACCATGACTAT 167
Db 1312 TGGTTAGTTAATCATATTTATTTTGTGTTTACGAGACCGATTAACATTAATGAT 1371
QY 168 GCGA 171
Db 1372 CCGA 1375
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RESULT 9
US-09-949-016-65898/c
; Sequence 65898, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65898
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-65898

Query Match 13.2%; Score 30.8; DB 4; Length 601;
Best Local Similarity 54.6%; Pred. No. 2;
Matches 59; Conservative 1; Mismatches 48; Indels 0; Gaps 0;
QY 2 TTTTGCAGTTAGTATATATGTTAGTGGCTCTATGATGAGTGAAGATTGACTTA 61
Db 376 TATTTCTTTTAAAGATATGTTACTTCTGTGTACAGCTGAAACATTTAAAAGA 317
QY 62 TTGATGAGCATCTCTGATGATGAGACTTCAGAAAAACATGACTCG 109
Db 316 AAAAAAGATGATGATGATGAGAAAAAAGAAATTAATTATTG 269
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RESULT 10
US-09-918-686-1/c
; Sequence 1, Application US/09318686
; Patent No. 6475739
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary
; APPLICANT: Proil, Sean
; APPLICANT: Paepfer, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; FILE REFERENCE: GENOMIC DELETIONS
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918,686
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 92139
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7043, 8369, 8401
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1
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Query Match 13.1%; Score 30.6; DB 4; Length 92139;
Best Local Similarity 68.9%; Pred. No. 23;
Matches 42; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 114 GCTACCGAGATTTATTTTATTTGCGATTCCTCATGCTACCATGATGATGAGGA 173
Db 71386 GCTGACATGATTCCTTGTCTGGAATTCCTCCATGAGGATCCATCCATCCTTGCTGTA 71327
QY 174 T 174
Db 71326 T 71326
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RESULT 11
US-09-949-016-16923
; Sequence 16923, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16923
; LENGTH: 390416
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16923

Query Match 13.1%; Score 30.6; DB 4; Length 390416;
Best Local Similarity 51.1%; Pred. No. 45;
Matches 72; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 13 AGTAGAATATGTTAGTGGCTCTATGATGAGTGAAGATTGATGATGAGGC 72
Db 98049 AGTAGAGTCTGTGGAGCTGAACAGTCCAGAGAAATCATCTCTTGAAGAGAGTG 98108
QY 73 AATCTGAGTATGAGCTTCAGAAAAACATGACTCGGAGAGCTACCGAGATTATTTTA 132
Db 98109 AGTGTGTAATTTAATCATCAGCAAGAACCTGTACTGAGAGCGAGAGAGCTGG 98168
QY 133 TTGGCATTCCTTCATGACT 153
Db 98169 TTCCAAATATTCCTCCTCAGT 98189
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RESULT 12
US-09-949-016-168377
; Sequence 168377, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 168377
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-168377

Query Match 13.0%; Score 30.2; DB 4; Length 601;
Best Local Similarity 60.2%; Pred. No. 3.2;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 122 AGATTATTTTATTTGGCATGCTCCATCAGTCACTACCTGATGCGAGATGATAGA 181
DB 211 AGACAAATATAAAGTGCATGACTCAAAAATTTACTTAAGATACCGTATGCTTAC 270

QY 182 TCATATTCATGATGCTCATCTTC 204
DB 271 CCTATGCTTTATTTAATCTTC 293

RESULT 13

US-09-949-016-12108/c
Sequence 12108, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12108

LENGTH: 14449

TYPE: DNA

ORGANISM: Human

US-09-949-016-12108

Query Match 13.0%; Score 30.2; DB 4; Length 14449;
Best Local Similarity 60.2%; Pred. No. 14;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 105 ACTCGGAGACTACCGAGATATTTATTTGGCATGCTCCATCAGTCTACCCATCAG 164
DB 5301 ACAAGTCACTATTGGTGGATTCCTTTAGCATTCCTCCATCAATGGTACATTAAG 5242

QY 165 TATGCGAGATGATAGATATAT 187
DB 5241 GATGCTCACAGATTAAGCACTAT 5219

RESULT 14

US-09-949-016-16483/c

Sequence 16483, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16483

LENGTH: 29628

TYPE: DNA

ORGANISM: Human

US-09-949-016-16483

Query Match 13.0%; Score 30.2; DB 4; Length 29628;
Best Local Similarity 60.2%; Pred. No. 19;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 122 AGATTATTTTATTTGGCATGCTCCATCAGTCACTACCCATCAGATGCGAGATGATAGA 181
DB 3410 AGACAAATATAAAGTGCATGACTCAAAAATTTACTTAAGATACCGTATGCTTAC 3351

QY 182 TCATATTCATGATGCTCATCTTC 204
DB 3350 CCTATGCTTTATTTAATCTTC 3328

RESULT 15

US-09-949-016-14856/c

Sequence 14856, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14856

LENGTH: 63385

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(63385)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14856

Query Match 12.9%; Score 30; DB 4; Length 63385;
Best Local Similarity 53.4%; Pred. No. 31;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 36 ATGATAGGATGGAAGATTTGATTTGATGAGGCAATCTGTAGATGAGACTTCAAG 95
DB 18045 ATGGAGGGATGCACTTTTAGAGGGGTGGGGAGGGCTTCACTAGAGAGGGGATTTG 17986

QY 96 AAACATGACTCGGGAAGCTACCGAGATTTATTTATTTGGCATGCTCCATCACT 153
DB 17985 CACAAAGACCGGAGGAGGCAAAATTTAAACGAAAGATTGCAATGCTTTAGCAGT 17928

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Thu May 5 18:28:54 2005

Job time : 76.1803 secs

us-09-300-482-1.rn1

Page 6

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 67.0098 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Issued Patents NA:
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4: /cgn2_6/pdata/1/ina/6B.COMB.seq:*
5: /cgn2_6/pdata/1/ina/PCTUS.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58.6	25.6	253	US-09-313-294A-6236	Sequence 6236, Ap
2	57.6	25.2	277	US-09-313-294A-4756	Sequence 4756, Ap
3	43.8	19.1	294	US-09-313-294A-5508	Sequence 5508, Ap
4	32.4	14.1	128516	US-09-949-016-13501	Sequence 13501, A
5	32.4	14.1	133157	US-09-949-016-12541	Sequence 12541, A
6	32	14.0	385	US-09-513-999C-23635	Sequence 23635, A
7	31.8	13.9	601	US-09-949-016-79076	Sequence 79076, A
8	31.8	13.9	163181	US-09-949-016-13730	Sequence 13730, A
9	31.8	13.9	211049	US-09-949-016-15770	Sequence 15770, A
10	31.8	13.9	784019	US-09-949-016-14033	Sequence 14033, A
11	31.8	13.9	828152	US-09-949-016-12777	Sequence 12777, A
12	31.6	13.6	7151	US-09-839-477-7	Sequence 7, Appl
13	31.2	13.6	2523	US-09-614-221A-346	Sequence 346, App
14	31.2	13.6	225127	US-09-949-016-16480	Sequence 16480, A
15	31.2	13.6	1830121	US-09-557-884-1	Sequence 1, Appl
16	31.2	13.6	1830121	US-09-643-990A-1	Sequence 1, Appl
17	31	13.5	601	US-09-949-016-195151	Sequence 195151, A
18	31	13.5	57331	US-09-949-016-17277	Sequence 17277, A
19	30.8	13.4	152583	US-09-949-016-12086	Sequence 12086, A
20	30.8	13.4	152583	US-09-949-016-17390	Sequence 17390, A
21	30.8	13.4	152583	US-09-949-016-17391	Sequence 17391, A
22	30.8	13.4	1230025	US-09-198-452A-1	Sequence 1, Appl
23	30.8	13.4	1230230	US-09-438-185A-1	Sequence 1, Appl
24	30.6	13.4	2454	US-09-248-796A-6173	Sequence 6173, Ap
25	30.6	13.4	640681	US-09-790-988-1	Sequence 1, Appl
26	30.4	13.3	1026	US-09-149-624-1	Sequence 1, Appl
27	30.4	13.3	15249	US-08-956-171B-102	Sequence 102, App

c	28	30.4	13.3	15249	4	US-08-781-986A-102	Sequence 102, App
c	29	30	13.1	286	4	US-09-313-294A-6591	Sequence 6591, Ap
c	30	30	13.1	400	3	US-09-222-938A-3	Sequence 3, Appl
c	31	29.6	12.9	996	4	US-09-328-352-3814	Sequence 3814, Ap
c	32	29.6	12.9	1152	3	US-09-134-001C-592	Sequence 592, App
c	33	29.6	12.9	1435	5	PCT-US95-05922A-1	Sequence 1, Appl
c	34	29.6	12.9	1601	4	US-09-023-655-497	Sequence 497, App
c	35	29.6	12.9	2580	2	US-08-511-485-7	Sequence 7, Appl
c	36	29.6	12.9	2580	4	US-09-201-936-7	Sequence 7, Appl
c	37	29.6	12.9	2580	4	US-09-011-356-7	Sequence 7, Appl
c	38	29.6	12.9	2580	4	US-09-672-717-222	Sequence 222, App
c	39	29.6	12.9	2580	4	US-09-201-932-7	Sequence 7, Appl
c	40	29.6	12.9	2589	3	US-08-569-749-1	Sequence 1, Appl
c	41	29.6	12.9	2589	4	US-09-689-366-1	Sequence 1, Appl
c	42	29.6	12.9	2589	4	PCT-US96-12860-1	Sequence 1, Appl
c	43	29.6	12.9	3516	5	US-09-710-279-3533	Sequence 3533, Ap
c	44	29.6	12.9	3532	2	US-09-205-204-1	Sequence 1, Appl
c	45	29.6	12.9	3732	3	US-09-212-971-7	Sequence 7, Appl

ALIGNMENTS

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RESULT 1
US-09-313-294A-6236
; Sequence 6236, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalqudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6236
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351460H1
US-09-313-294A-6236

Query Match      25.6%; Score 58.6; DB 4; Length 253;
Best Local Similarity 66.4%; Pred. No. 2.4e-10;
Matches: 99; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY      65 ACAGAAATAGCGCTTGTGATGCGCTGTATATGGGCAAAATCTGGCACTCAATATTGCT 124
DB      82 ACAGAAATCGGCTTGTGATGCGCTTGTGATGCGGCAAGGCAAGCTTGCCTCAATTTGCA 141

QY      125 TGAAGAGGCTTCCCAATTCGGTTAACAAGCAACCATTTCCAGGTTATTTGGCCATA 184
DB      142 GAGAAAGGG-TTCCCATCTCTGTGTACACAGCAACCTTCAGGTGAGACGACGCT 200

QY      185 AGACGAGCAAAACGAGGAAGAACTTC 213
DB      201 GAGCGCTGCCAAGGACGAGAAAGAACTTC 229

RESULT 2
US-09-313-294A-4756
; Sequence 4756, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalqudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US

```

/ CURRENT APPLICATION NUMBER: US/09/313,294A
 / CURRENT FILING DATE: 1999-05-14
 / NUMBER OF SEQ ID NOS: 7600
 / SOFTWARE: PERL Program
 / SEQ ID NO 4756
 / LENGTH: 277
 / TYPE: DNA
 / ORGANISM: Zea mays
 / FEATURE:
 / NAME/KEY: misc feature
 / OTHER INFORMATION: Incyte ID No. 6476212 700348987H1
 / LOCATION: 2, 72, 88
 / OTHER INFORMATION: a, t, c, g, or other
 US-09-313-294A-4756

Query Match 25.2%; Score 57.6; DB 4; Length 277;
 Best Local Similarity 65.8%; Pred. No. 5.5e-10;
 Matches 98; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

QY 65 ACAAGATAGGCTTGTGATGCTGTTAATGGGCAAAATCTGCACATCATATTGCT 124
 DB 82 ACAAGATCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 141
 QY 125 TGAAGAGGCTTCCCAATTCGGTTAAACGGAACCATTTCCAGGTTATGGGCGAT 184
 DB 142 GAGAAAGGG-TTCCCATCTCTGTGTACAAAGAACCTCCAGGTGACGAGACCGT 200
 QY 185 AGACGAGCAACCAAGGAGAAACCTTC 213
 DB 201 GACGCTGCCAAGGACGAGAAACCTTC 229

RESULT 3
 US-09-313-294A-5508
 / Sequence 5508, Application US/09313294A
 / Patent No. 6476212
 / GENERAL INFORMATION:
 / APPLICANT: Ialsudi, Raghunath V.
 / APPLICANT: Ito, Laura Y.
 / APPLICANT: Sherman, Bradley K.
 / TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 / FILE REFERENCE: PL-0017 US
 / CURRENT APPLICATION NUMBER: US/09/313,294A
 / CURRENT FILING DATE: 1999-05-14
 / NUMBER OF SEQ ID NOS: 7600
 / SOFTWARE: PERL Program
 / SEQ ID NO 5508
 / LENGTH: 294
 / TYPE: DNA
 / ORGANISM: Zea mays
 / FEATURE:
 / NAME/KEY: misc feature
 / OTHER INFORMATION: Incyte ID No. 6476212 700350270H1
 / NAME/KEY: unsure
 / LOCATION: 51
 / OTHER INFORMATION: a, t, c, g, or other
 US-09-313-294A-5508

Query Match 19.1%; Score 43.8; DB 4; Length 294;
 Best Local Similarity 60.4%; Pred. No. 3.4e-05;
 Matches 90; Conservative 0; Mismatches 57; Indels 2; Gaps 1;

QY 75 GCCTTGCTGATTTGCTGTTAATGGGCAAAATCTGCACATCATATTGCTGAAAAAGGC 134
 DB 145 GCCTGCGCGGCTGCGGTGATGAGACAGAACCTTGCCTCAACATGCGGAGAAAGGT 204
 QY 135 TTCCCAATTCGGGTTAAACAGCAACCATTTCCAGGTTATGGGCGCATTAAGCAAGCA 194
 DB 205 TCCCAATTCGGGTTAAACAGCA--CAACTCCAAAGGTGATGAGACCGTGCAGCGGTCC 262
 QY 195 AACGAGAGAAACCTTCATTTATGGG 223

DB 263 AAGTCGAGAGAACTCCCAAGTGTGG 291

RESULT 4
 US-09-949-016-13501
 / Sequence 13501, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / CURRENT FILING DATE: 2000-04-14
 / PRIOR APPLICATION NUMBER: 60/241,755
 / PRIOR FILING DATE: 2000-10-20
 / PRIOR APPLICATION NUMBER: 60/237,768
 / PRIOR FILING DATE: 2000-10-03
 / PRIOR APPLICATION NUMBER: 60/231,498
 / PRIOR FILING DATE: 2000-09-08
 / NUMBER OF SEQ ID NOS: 207012
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 13501
 / LENGTH: 128516
 / TYPE: DNA
 / ORGANISM: Human
 US-09-949-016-13501

Query Match 14.1%; Score 32.4; DB 4; Length 128516;
 Best Local Similarity 48.9%; Pred. No. 6.4;
 Matches 87; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 26 CTTCAATTCAGAGATTAATTTGCGCTCAACCCACACAGAAATAGCCCTTGCTGCA 85
 DB 16045 CTTGATACCTGACCAAGTATGAGAAATGATCCGCTCATGTGCTGTTA 16104
 QY 86 TTGCTGTTAATGGGCAAAATCTGGCACTCAATTTGCTTGAAGGGCTTCCCAATTCG 145
 DB 16105 GTGAGAGGAATGCAAAATTAATGCTCTGCTATTCTTAAGGAAGGCTTGCCTCAAGGTC 16164
 QY 146 GGTAAACAGGAACCAATTCCTCAAGTTATGCGGCAATAGAGAGCAACCAAGAA 203
 DB 16165 ATGCACACAGTGGCAATGTAATTTTAAACTGACGAGATTTGAAACATGTGTA 16222

RESULT 5
 US-09-949-016-12541
 / Sequence 12541, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / CURRENT FILING DATE: 2000-04-14
 / PRIOR APPLICATION NUMBER: 60/241,755
 / PRIOR FILING DATE: 2000-10-20
 / PRIOR APPLICATION NUMBER: 60/237,768
 / PRIOR FILING DATE: 2000-10-03
 / PRIOR APPLICATION NUMBER: 60/231,498
 / PRIOR FILING DATE: 2000-09-08
 / NUMBER OF SEQ ID NOS: 207012
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 12541
 / LENGTH: 133157
 / TYPE: DNA
 / ORGANISM: Human
 US-09-949-016-12541

Query Match 14.1%; Score 32.4; DB 4; Length 133157;
 Best Local Similarity 48.9%; Pred. No. 6.5;
 Matches 87; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 26 CTTCATTTTCAGAGATTAATATGCGCTCAACCCACAGACAGATAGCGCTTGCGA 85
 DB 16031 CTTCATTTTCAGAGATTAATATGCGCTCAACCCACAGAGATAGCGCTTGCGA 16090
 QY 86 TTGGCTGTTAATGGGCAAAATCTGGCACTCATATTTGCTGAAAGGGCTTCCCAATTC 145
 DB 16091 GTGGAAGGAAATGTGCAATTTATGCTGCTATTTCTAACTGAAAGAGACTTGGCCAGGTC 16150
 QY 146 GGTTAACAACGAGAACCATTTCCAGGTTATTTGGCGATTAAGAAGCAACAGCAAGAA 203
 DB 16151 ATGCAACAAGTTGGCAATGTAATATTTTAAACTGAGACAGATGTTGAATAATGTA 16208
 RESULT 6
 US-09-513-999C-23635
 ; Sequence 23635, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6783961
 ; FILE REFERENCE: 59, US2, REG
 ; CURRENT APPLICATION NUMBER: US/09/513, 999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 23635
 ; LENGTH: 385
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 13
 ; OTHER INFORMATION: w=a or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 98
 ; OTHER INFORMATION: n=a, g, c or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 99
 ; OTHER INFORMATION: h=a or c or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 151
 ; OTHER INFORMATION: m=a or c
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 152
 ; OTHER INFORMATION: m=a or c
 ; US-09-513-999C-23635
 Query Match 14.0%; Score 32; DB 4; Length 385;
 Best Local Similarity 51.4%; Pred. No. 0.48;
 Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
 QY 9 ATTTTTCGTGATTCCTTCAAAATTCAGAGATTAATATGCGCTCAACCCACAGAA 68
 DB 242 ATTTTTCGTGATTCCTTCAAAATTCAGAGATTAATATGCGCTCAACCCACAGAA 301
 QY 69 GAATAGCGCTTGTGATTCCTTCAAAATTCAGAGATTAATATGCGCTCAACCCACAGAA 128
 DB 302 GAATAGCGCTTGTGATTCCTTCAAAATTCAGAGATTAATATGCGCTCAACCCACAGAA 361
 QY 129 AAGGCTTCCCAATTCGGTTAAC 152
 DB 362 AGTGAGATTCGAATATGCTTAAAC 385

RESULT 7
 US-09-949-016-79076/c
 ; Sequence 79076, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 79076
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-79076
 Query Match 13.9%; Score 31.8; DB 4; Length 601;
 Best Local Similarity 64.0%; Pred. No. 0.71;
 Matches 48; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 QY 2 AGACCTTATTTTCTGATTCCTTCAAAATTCAGAGATTAATATGCGCTCAACCC 61
 DB 528 AAGGAGATTTTCTGATTCCTTCAAAATTCAGAGATTAATATGCGCTCAACCC 469
 QY 62 ACAACAGATAGGC 76
 DB 468 ACACTGAATAGC 454
 RESULT 8
 US-09-949-016-13730
 ; Sequence 13730, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13730
 ; LENGTH: 163181
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(163181)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-949-016-13730
 Query Match 13.9%; Score 31.8; DB 4; Length 163181;
 Best Local Similarity 53.7%; Pred. No. 12;
 Matches 66; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
 QY 103 AATCTGCACTCATATTTGCTGAAAGGGCTTCCCAATTCGGTTAACAAGAGACA 162

Db 140224 AATTTGAGGTGATCTATGTAATGAAAGTCTGCAATTTATGCGGCAACACACGAGG 140283
QY 163 TTTCAGAGTTATTGGGCCATTAAGACGAAGCAACAGAGAAAGAACTTCAATTTATGG 222
Db 140284 CTGAAACAGATTATTAGACAGATACAGAGGACCAAGGAAAGAACTGCAATGAGG 140343
QY 223 GGA 225
Db 140344 AGA 140346

RESULT 9
US-09-949-016-15770/C
; Sequence 15770, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 15770
; LENGTH: 211049
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15770

Query Match
Best Local Similarity 13.9%; Score 31.8; DB 4; Length 211049;
Matches 81; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 2 AGACCTTATTTTCTGTCATTTGCTCAATTTTCAGAGATTAATTAATGCGCTCAACCC 61
Db 22914 AATGTTGATTAATAGAGGCTTTGTACAAATTTGAGAAATGAGGCACTGCTTAGTGC 22855
QY 62 ACAACAGAAATGAGGCTTCTGATTCGCTGTAATGAGCAAAATCTGCACTCAATAT 121
Db 22854 AAAATGTTGATTTTACAACTAGATTGGCTTATATTTGGTAAATAATTCGACGATA 22795
QY 122 GCTTGAAGAGGCTTCCCAATTCGGTTTACAAAGCAACCAATT 164
Db 22794 ATTTCAAATGATTCACATTTATGGTAAACATTTACCACT 22752

RESULT 10
US-09-949-016-14033/C
; Sequence 14033, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 14033
; LENGTH: 784019
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(784019)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14033

Query Match
Best Local Similarity 13.9%; Score 31.8; DB 4; Length 784019;
Matches 48; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2 AGACCTTATTTTCTGTCATTTGCTCAATTTTCAGAGATTAATTAATGCGCTCAACCC 61
Db 474638 AAGCAGAAATTTTCTTAGATTGCTTCAATTTGGAATTAATATGTGTGGCTCAATAT 474579
QY 62 ACAACAGAAATGAGC 76
Db 474578 ACACTGAATATGAC 474564

RESULT 11
US-09-949-016-12777/C
; Sequence 12777, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12777
; LENGTH: 828152
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(828152)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12777

Query Match
Best Local Similarity 13.9%; Score 31.8; DB 4; Length 828152;
Matches 48; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2 AGACCTTATTTTCTGTCATTTGCTCAATTTTCAGAGATTAATTAATGCGCTCAACCC 61
Db 470771 AAGCAGAAATTTTCTTAGATTGCTTCAATTTGGAATTAATATGTGTGGCTCAATAT 470712
QY 62 ACAACAGAAATGAGC 76
Db 470711 ACACTGAATATGAC 470697

RESULT 12
US-09-839-477-7
; Sequence 7, Application US/09839477
; Patent No. 6723895
; GENERAL INFORMATION:
; APPLICANT: Shorttosh, Basil S.
; APPLICANT: DeBonte, Lorin R.
; TITLE OF INVENTION: PLANTS CONTAINING A CYTOSOLIC ACETYL

;; TITLE OF INVENTION: COA-CARBOXYLASE
;; FILE REFERENCE: 07148-094001
;; CURRENT APPLICATION NUMBER: US/09/839,477
;; CURRENT FILING DATE: 2001-04-20
;; PRIOR APPLICATION NUMBER: US 60/198,794
;; PRIOR FILING DATE: 2000-04-20
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 7
;; LENGTH: 7151
;; TYPE: DNA
;; ORGANISM: Medicago sativa
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(6771)
US-09-839-477-7

Query Match 13.8%; Score 31.6; DB 4; Length 7151;
Best Local Similarity 54.2%; Pred. No. 2.9;
Matches 64; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 54 CTCACCCCAACAAGATAGGCTTGTGATGGCTGTTAATGGCAAAATCTGGCAC 113
DB 5807 CTGATTCGCGACCAAGCGCCCAAGCATATTGATTTCAACAGAGAAGACTCCAC 5866

QY 114 TCAATATTCCTGAAAAGGCTTCCCAATTCGGTTAACAACGGAACATTTCCAAAG 171
DB 5867 TTTTCATTATCCCAACTGAGAGGCTTTTCAGGTGAGCAAGGACCTTTTGAAGG 5924

RESULT 13
US-09-614-221A-346
; Sequence 346, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasubramanian
; APPLICANT: Yu, Jaehyun
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 346
; LENGTH: 2523
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-346

Query Match 13.6%; Score 31.2; DB 4; Length 2523;
Best Local Similarity 55.6%; Pred. No. 2.3;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 69 GATAGGCTTCTGATGCTGTTAATGGCAAAATCTGGCACTCAATATTGCTTGA 128
DB 2305 GGATGGGACTTCTGATGCTGTTAATGATGACGCAAAATGTAATATTACCAATTTTG 2364

QY 129 AAGGCTTCCCAATTCGGTTAACAACGGAACATTTCCAAAGTTATT 176
DB 2365 AAGGCTCACAATTCATGAAAACAAGGTAAGATCAACAAGTTATT 2412

RESULT 14
US-09-949-016-16480
; Sequence 16480, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 16480
;; LENGTH: 225127
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1)...(225127)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16480

Query Match 13.6%; Score 31.2; DB 4; Length 225127;
Best Local Similarity 54.3%; Pred. No. 22;
Matches 63; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 93 TTAATGGCAAAATCTGGCACTCAATATTGCTTGAAGGCTTCCCAATTCGGTTAAC 152
DB 16067 TTTAAAAGACAGACAGCTAGCTAGATTAATAAGACCAAGCCCAATTTGCTCTTTC 16126

QY 153 AAGGACCAATTTCCAAAGTTATTGGGCAATTAAGACGAAGCAACAGAGAGAA 208
DB 16127 ATGAGACCAATTTCAATGATTAATGTATCCACAGCGCAAGTAAAGAGATGAGAG 16182

RESULT 15
US-09-557-884-1/C
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleisemann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs

```

:      TYPE: nucleic acid
:      STRANDEDNESS: double
:      TOPOLOGY: linear
:      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

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Query Match	13.6%	Score 31.2;	DB 4;	Length 1830121;
Best Local Similarity	53.2%;	Pred. No. 60;		
Matches 66;	Conservative 0;	Mismatches 58;	Indels 0;	Gaps 0;

QY	31	TATTTACAGAGTGTATATTGGGCTCAACCCCAACAAATAATAGGCTTGCTGGATTTGGC	90
Db	324697	ACTTTTATATAAAAAATTTTACTTGATACAAATTTAGAAATTTGCTTTTGAGATTTCTC	324638
QY	91	TGTTAATGGGCAAAATCTGGCACTCAATATTTGCTTGAAAGAGGCTTCCCAATTTCCGGTTA	150
Db	324637	TATTTATTTGGCGATACATATATCTCAAAATTTAGTTGAGCGGATTTTGCTCTCAAAATTTG	324578
QY	151	ACAA 154	
Db	324577	ACAA 324574	

Search completed: May 4, 2005, 12:28:02
Job time : 75.0098 secs

11	62.8	27.4	234	11	US-09-732-627A-2087	Se
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11	62.8	27.4	234	11	US-09-732-627A-2087	Sequence 2087, Ap
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Db 2390 CTCACAGAATAGGCTTGCTGACTGGCTGTTATGGCCAAATCTAGCACTCAATAT 244

QY 121 TGCTGAAAAGGCTTCCCAATTCGGTTACAGAGAACATTTCCAAGTTATTGGGC 180
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Db 2450 TGC-TGAGAAAGGCTTCCCATTTCTGTTTATACCGAACCACTTCCAAAGTTATGAGA 2508
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QY 181 CATAAGACGAAGCAACGAGAAAGAACTTTCATTTATGGGACAA 229
|||
Db 2509 CTGTGAAACGAGCAAAACAGAAAGAAATCTTCCAGTTATGGCTACCA 2557
|||

RESULT 2

US-10-424-599-59924
; Sequence 59924, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 59924
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25122C.1
US-10-424-599-59924

Query Match 59.5%; Score 136.2; DB 17; Length 2691;
Best Local Similarity 80.3%; Pred. No. 2, 5e-33;
Matches 184; Conservative 0; Mismatches 43; Indels 2; Gaps 2;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTAATATGGCTCAACC 60
|||
Db 269 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTAATATGGCTCAACC 327
|||
QY 61 CACAAACAGAAATAGGCTTCCCAATTCGGTTATGGGCAAAATCTGGCACTCAAT 120
|||
Db 328 CTCACAGAAATAGGCTTCCCAATTCGGTTATGGGCAAAATCTGGCACTCAAT 387
|||
QY 121 TGCTGAAAAGGCTTCCCAATTCGGTTATGGGCAAAATCTGGCACTCAAT 180
|||
Db 388 TGC-TGAGAAAGGCTTCCCATTTCTGTTTATACCGAACCACTTCCAAAGTTATGAGA 446
|||
QY 181 CATAAGACGAAGCAACGAGAAAGAACTTTCATTTATGGGACAA 229
|||
Db 447 CTGTGAAACGAGCAAAACAGAAAGAAATCTTCCAGTTATGGCTACCA 495
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RESULT 3

US-10-424-599-59920
; Sequence 59920, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 59920
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Glycine max

FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(578)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_25119C.1
US-10-424-599-59920

Query Match 55.3%; Score 126.6; DB 17; Length 578;
Best Local Similarity 77.7%; Pred. No. 1, 6e-30;
Matches 178; Conservative 0; Mismatches 49; Indels 2; Gaps 2;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTAATATGGCTCAACC 60
|||
Db 216 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTAATATGGCTCAACC 274
|||
QY 61 CACAAACAGAAATAGGCTTCCCAATTCGGTTATGGGCAAAATCTGGCACTCAAT 120
|||
Db 275 CTCACAGAAATAGGCTTCCCAATTCGGTTATGGGCAAAATCTGGCACTCAAT 334
|||
QY 121 TGCTGAAAAGGCTTCCCAATTCGGTTATGGGCAAAATCTGGCACTCAAT 180
|||
Db 335 TGC-TGAGCAAGGCTTCCCATTTCTGTTTATACCGAACCACTTCCAAAGTTATGAGA 393
|||
QY 181 CATAAGACGAAGCAACGAGAAAGAACTTTCATTTATGGGACAA 229
|||
Db 394 CTGTGAAACGAGCAAAACAGAAAGAAATCTTCCAGTTATGGCTACCA 442
|||

RESULT 4

US-10-425-114-12849
; Sequence 12849, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12849
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701214664_FLI
US-10-425-114-12849

Query Match 51.1%; Score 117; DB 17; Length 1737;
Best Local Similarity 81.2%; Pred. No. 3, 5e-27;
Matches 160; Conservative 0; Mismatches 35; Indels 2; Gaps 2;

QY 33 TTTCAGAGATTAATATTCGCTCAACCCACAAAGAAATAGGCTTCTGGATTTGGCTG 92
|||
Db 43 TATCTTGAGATTAATATATG-GCTCAACCCACAAAGAAATAGGCTTCTGGATTTGGCTG 101
|||
QY 93 TTATAGGCAAAATCTGGCACTCAATTTGCTTGAAGGGCTTCCCAATTCGGTTAAC 152
|||
Db 102 TTATAGGCAAAATCTGGCACTCAATTTGCTTGAAGGGCTTCCCAATTCGGTTAAC 160
|||
QY 153 AACGAAACATTTCCAAAGTTATGGGCAATAGAGCAAGAAACGAGAAAGAACTT 212
|||
Db 161 AACGAAACATTTCCAAAGTTATGGGCAATAGAGCAAGAAACGAGAAAGAACTT 220
|||
QY 213 CAATTTATGGGCAAA 229
|||
Db 221 CCAATTTATGGCTACCA 237
|||

RESULT 5
US-10-425-114-10641
; Sequence 10641, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10641
; LENGTH: 1627
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700954712_FLI
US-10-425-114-10641

Query Match 35.4%; Score 81; DB 17; Length 1627;
Best Local Similarity 72.1%; Pred. No. 1.7e-15;
Matches 119; Conservative 0; Mismatches 45; Indels 1; Gaps 1;

QY 65 ACAAGATGGCTTCTGATGTTGGTGAATGGCAAAATCTGGCACTCAATATGCT 124
DB 71 ACAAGATGGCTTCTGATGTTGGTGAATGGCAAAATCTGGCTCAACATTCG- 129

QY 125 TGAAGAGGCTTCCCAATTCGGTTAAACAAGGAACCATTTTCAAGGTATTGGCCATA 184
DB 130 TGAGAAAGGCTTCCCAATTCCTGTTCTACACCGGACCGGCTCCAGGTTGATGACAGT 189

QY 185 AGACGAGCAACCAAGAGGAACCTTCATTTATGGGAAACA 229
DB 190 TGAAGAGCAAAACAAGAGGAACCTTCCTGTGTATGCTACCA 234

RESULT 6
US-10-424-599-76904
; Sequence 76904, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 76904
; LENGTH: 1838
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40459C.1
US-10-424-599-76904

Query Match 35.4%; Score 81; DB 17; Length 1838;
Best Local Similarity 72.1%; Pred. No. 1.8e-15;
Matches 119; Conservative 0; Mismatches 45; Indels 1; Gaps 1;

QY 65 ACAAGATGGCTTCTGATGTTGGTGAATGGCAAAATCTGGCACTCAATATGCT 124
DB 71 ACAAGATGGCTTCTGATGTTGGTGAATGGCAAAATCTGGCTCAACATTCG- 129

DB 224 ACAAGATAGGCTTGTGCTGAGCTGATGAGGCCAAACCTTCTCTCAACATTCG- 282

QY 125 TGAAGAGGCTTCCCAATTCGGTTAAACAAGGAACCATTTCCAGGTATTGGCCATA 184
DB 283 TGAGAAAGGCTTCCCAATTCCTGTTCTACAAACCGGACCGGCTCCAGGTTGATGACAGT 342

QY 185 AGACGAGCAACCAAGAGGAACCTTCATTTATGGGAAACA 229
DB 343 TGAAGAGCAAAACAAGAGGAACCTTCCTGTGTATGCTACCA 387

RESULT 7
US-10-739-930-1129
; Sequence 1129, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 1129
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: ARATH-23APR03-CLUSTER6852_1
US-10-739-930-1129

Query Match 32.4%; Score 74.2; DB 18; Length 1785;
Best Local Similarity 68.4%; Pred. No. 2.9e-13;
Matches 117; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

QY 53 GCTCAACCAACAAGATAGGCTTCTGATGTTGGCTTTATGGCAAAATCTGCGA 112
DB 110 GCTGTTCAACCTACAAAGATAGGCTTAGCTGACTGCTGATGGGTACAACTAGT 169

QY 113 CTCATATTTGCTTGAAGAGGCTTCCCAATTCGGTTAAACAAGGAACCATTTCCAGGT 172
DB 170 CTCATATTTGCA-GAGAAAGGCTTCCCAATTCCTGTTTACAAAGAACTTCCAAAGT 228

QY 173 TATTGGCCATTAAGACGAGCAACCAAGAGGAACCTTCATTTATGGG 223
DB 229 TGATGAGACCGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 279

RESULT 8
US-10-424-599-98726
; Sequence 98726, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 98726
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_60162C.1
US-10-424-599-98726

Query Match 32.2%; Score 73.8; DB 17; Length 375;
Best Local Similarity 63.2%; Pred. No. 1.9e-13;

Query Match	26.3%	Pred. 60.2;	DB 18;	Length 1831;
Best Local Similarity	64.2%;	Fred. No. 1.1e-08;		
Matches 106;	Conservative 0;	Mismatches 58;	Indels 1;	Gaps. 1#
QY	65	ACAAGAAATAGCCCTTGCTGTGATTTGGCTTTATGGGCAAAATCTGGACTCAATATTGCT	124	
Db	88	ACTGAATATGCTCTTGCTGCGCTTGCGGCTCATGGGCGAAGACCTTGCCCTCAACATTGCA	147	
OY	125	TGAAGAGGCTTCCCAATTCCGGTTACACGAGCAACATTTCCAAAGTTAATTGGGCCATA	184	

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; LENGTH:637
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT1577_183003C.1
US-10-425-115-91011
Query Match      25.6%; Score 58.6; DB 18; length 637

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Best Local Similarity 66.4%; Pred. No. 2.1e-08;
 Matches 99; Conservative 0; Mismatches 49; Indels 1; Gaps 1;
 QY 65 ACAAGAAATAGGCTTGTGCTGATTTGCTGTTATGGGCAAAATCTGGCACTCAATATTGCT 124
 Db 164 ACAAGAAATCGGTCTTGTGCTGCTGCGCTCATGGGCGAAGAACTTGCCCTCAACATTGCA 223
 QY 125 TGAAGAGGCTTCCCAATTCCGGTTAAACGAAACCAATTTCAGGTTAATGGCCATA 184
 Db 224 GAGAAAGGG-TTCCCACTCTGTGTACAAACAGACAACTCCAAAGGTGAGCGAGACCGT 282
 QY 185 AGACGAAGCAAAACGAGAGGAACCTTC 213
 Db 283 GCACCGTCCCAAGGCAAGAAACCTTC 311

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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SUMMARIES

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4	229	100.0	229	21	US-09-371-146A-181981
5	229	100.0	229	26	US-09-552-086-26409
6	229	100.0	229	29	US-09-654-617-43713
7	229	100.0	229	31	US-09-684-016-43713
8	229	100.0	229	45	US-09-985-678-181981
9	161.4	70.5	305	77	US-09-089-810-829
10	153.8	67.2	261	20	US-09-300-482-70
11	153.8	67.2	261	20	US-09-304-517A-109274
12	153.8	67.2	261	21	US-09-371-146A-109274
13	153.8	67.2	261	45	US-09-985-678-109274
14	153.8	67.2	447	37	US-09-874-708A-16025
15	153.8	67.2	447	37	US-09-874-708A-16025
16	153.8	67.2	497	30	US-09-211-750-15882
17	153.8	67.2	497	90	US-09-874-708A-18187
18	152.8	66.7	262	18	US-09-211-750-18044
19	152.8	66.7	262	44	US-09-244-000A-14731
20	152.2	66.5	259	20	US-09-978-703-14731
21	152.2	66.5	259	20	US-09-300-482-74
22	152.2	66.5	259	20	US-09-304-517A-133493
23	152.2	66.5	259	21	US-09-371-146A-133493
24	152.2	66.5	259	45	US-09-985-678-133493
25	152.2	66.5	479	37	US-09-874-708A-22353
26	151.8	66.3	259	18	US-09-211-750-22158
27	151.8	66.3	259	18	US-09-244-000A-70591
28	151.4	66.1	275	18	US-09-978-703-70591
29	151.4	66.1	275	20	US-09-244-000A-21474
30	151.4	66.1	275	20	US-09-300-482-66
31	151.4	66.1	275	20	US-09-304-517A-289993
32	151.4	66.1	275	21	US-09-371-146A-286774
33	151.4	66.1	275	44	US-09-978-703-21474
34	151.4	66.1	275	45	US-09-985-678-289993
35	151	65.9	281	20	US-09-300-482-82
36	151	65.9	281	20	US-09-304-517A-184827
37	151	65.9	281	21	US-09-371-146A-184827
38	149.8	65.4	374	45	US-09-985-678-184827
39	149.8	65.4	374	20	US-09-304-517A-235976
40	149.8	65.4	374	21	US-09-371-146A-235976
41	149.8	65.4	374	21	US-09-391-530-5396
42	149.8	65.4	374	27	US-09-615-060A-10170
43	149.8	65.4	374	45	US-09-985-678-235976
44	149.8	65.4	399	20	US-09-144-084-32994
45	149.4	65.2	281	18	US-09-300-482-103
					US-09-244-000A-74679

ALIGNMENTS

```
RESULT 1
US-09-300-482-27
; Sequence 27, Application US/09300482
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Peschke, Virginia M.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE REFERENCE: 04993.0031.US01/38-21 (15365) B
; CURRENT APPLICATION NUMBER: US/09/300,482
; NUMBER OF SEQ ID NOS: 699
; SEQ ID NO 27
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Glycine max
US-09-300-482-27
```

Query Match 100.0%; Score 229; DB 20; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTATATGCGTCAACC 60
DB 1 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTATATGCGTCAACC 60
QY 61 CACACAGAAATAGGCTTGCTGCGATTGCGTGAATGGCAAAATCTGCACTCAATAT 120
DB 61 CACACAGAAATAGGCTTGCTGCGATTGCGTGAATGGCAAAATCTGCACTCAATAT 120
QY 121 TGCTTGAAGAGGCTTCCCAATTCGGTTAACACGAACTTTCAGAGTTATGGGC 180
DB 121 TGCTTGAAGAGGCTTCCCAATTCGGTTAACACGAACTTTCAGAGTTATGGGC 180
QY 181 CATTAAGACGAACAAACCGAAGAAACCTTCAATTTATGGGAACAA 229
DB 181 CATTAAGACGAACAAACCGAAGAAACCTTCAATTTATGGGAACAA 229
```

```
RESULT 2
US-09-304-517A-181981
; Sequence 181981, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21 (15097) B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 181981
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-181981
```

Query Match 100.0%; Score 229; DB 20; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTATATGCGTCAACC 60
DB 1 CAGACCTTATTTTCTGTCATTTGCTTCAATTTGAGAGATTATATGCGTCAACC 60
QY 61 CACACAGAAATAGGCTTGCTGCGATTGCGTGAATGGCAAAATCTGCACTCAATAT 120
DB 61 CACACAGAAATAGGCTTGCTGCGATTGCGTGAATGGCAAAATCTGCACTCAATAT 120
QY 121 TGCTTGAAGAGGCTTCCCAATTCGGTTAACACGAACTTTCAGAGTTATGGGC 180
DB 121 TGCTTGAAGAGGCTTCCCAATTCGGTTAACACGAACTTTCAGAGTTATGGGC 180
```


Query Match	100.0%;	Score 229;	DB 21;	length 229;
Best Local Similarity	100.0%;	Pred. No. 1.3e-60;		
Matches	229;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
QY	1	CAGACCTATTATTTCTCTCATTTGCTTCCAATTTCAGAGACTTATATATAGGCGTCAACC	60	
		1	CAGACCTATTATTTCTCTCATTTGCTTCCAATTTCAGAGACTTATATATAGGCGTCAACC	60
Db	1	CAGACCTATTATTTCTCTCATTTGCTTCCAATTTCAGAGACTTATATATAGGCGTCAACC	60	

	Query Match	100.0%	Score 229;	DB 26;	length 229;
	Best Local Similarity	100.0%	Pred. No. 1,3e-60;		
	Matches 229;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	CAGACCTTATTTTTTCTGTCAATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAAC	60		
Db	1	CAGACCTTATTTTTTCTGTCAATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAAC	60		
Qy	61	CACAACAAATATAGGCGTGTCTGCAATTTGGCGTTAATGGCGAAATCTGGCACTCAATAT	120		
Db	61	CACAACAAATATAGGCGTGTCTGCAATTTGGCGTTAATGGCGAAATCTGGCACTCAATAT	120		
Qy	121	TGCTTGAAGGAGGCTTCCCAATTCGCGTTAACACGAGACATTTCCAGGTTATTTGGG	180		
Db	121	TGCTTGAAGGAGGCTTCCCAATTCGCGTTAACACGAGACATTTCCAGGTTATTTGGG	180		
Qy	181	CATTAGACGACCAACACGAGAGGAACCTTCAATTTATGGGGAACA	229		
Db	181	CATTAGACGACCAACACGAGAGGAACCTTCAATTTATGGGGAACA	229		

```

RESULT 6
US-09-654-617-43713
; Sequence 43713, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Liu, Kowalcic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(150977)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 43713
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Glycine max
US-09-654-617-43713

Query Match      100.0%   Score 229,   DB 29,   Length 229

```

Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
DB 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
QY 61 CACAACAGAAATAGGCGCTTCTGATTTGCTTAAATGGGCAAAATCTGGCACTCAATAT 120
DB 61 CACAACAGAAATAGGCGCTTCTGATTTGCTTAAATGGGCAAAATCTGGCACTCAATAT 120
QY 121 TGGTTGAAAAGGGCTTCCCAATTCGGTTACACAGAACCATTTCCAGTTATTGGGC 180
DB 121 TGGTTGAAAAGGGCTTCCCAATTCGGTTACACAGAACCATTTCCAGTTATTGGGC 180
QY 181 CATTAAGACGAAGCAACCAAGAAAGAAACCTTCAATTTATGGGAAACA 229
DB 181 CATTAAGACGAAGCAACCAAGAAAGAAACCTTCAATTTATGGGAAACA 229

RESULT 7
US-09-684-016-43713
; Sequence 43713, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; NUMBER OF SEQ ID NOS: 2000-09-05
; SEQ ID NO 43713
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Glycine max
US-09-684-016-43713

Query Match 100.0%; Score 229; DB 31; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
DB 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
QY 61 CACAACAGAAATAGGCGCTTCTGATTTGCTTAAATGGGCAAAATCTGGCACTCAATAT 120
DB 61 CACAACAGAAATAGGCGCTTCTGATTTGCTTAAATGGGCAAAATCTGGCACTCAATAT 120
QY 121 TGGTTGAAAAGGGCTTCCCAATTCGGTTAACAAGAACCATTTCCAGTTATTGGGC 180
DB 121 TGGTTGAAAAGGGCTTCCCAATTCGGTTAACAAGAACCATTTCCAGTTATTGGGC 180
QY 181 CATTAAGACGAAGCAACCAAGAAAGAAACCTTCAATTTATGGGAAACA 229
DB 181 CATTAAGACGAAGCAACCAAGAAAGAAACCTTCAATTTATGGGAAACA 229

RESULT 8
US-09-985-678-181981
; Sequence 181981, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517,255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529

; SEQ ID NO 181981
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-181981

Query Match 100.0%; Score 229; DB 45; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
DB 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTATGCGCTCAACC 60
QY 61 CACAACAGAAATAGGCGCTTCTGATTTGCTTAAATGGGCAAAATCTGGCACTCAATAT 120
DB 61 CACAACAGAAATAGGCGCTTCTGATTTGCTTAAATGGGCAAAATCTGGCACTCAATAT 120
QY 121 TGGTTGAAAAGGGCTTCCCAATTCGGTTAACAAGAACCATTTCCAGTTATTGGGC 180
DB 121 TGGTTGAAAAGGGCTTCCCAATTCGGTTAACAAGAACCATTTCCAGTTATTGGGC 180
QY 181 CATTAAGACGAAGCAACCAAGAAAGAAACCTTCAATTTATGGGAAACA 229
DB 181 CATTAAGACGAAGCAACCAAGAAAGAAACCTTCAATTTATGGGAAACA 229

RESULT 9
US-60-089-810-829
; Sequence 829, Application US/60089810
; GENERAL INFORMATION:
; APPLICANT: Joseph R. Byrum
; APPLICANT: Michael D. Thompson
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules
; TITLE OF INVENTION: Associated With Plants.
; NUMBER OF SEQUENCES: 5409
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lawrence M. Lavin, Jr.
; STREET: B&F
; STREET: Monsanto Company
; STREET: 700 Chesterfield Parkway North
; CITY: St. Louis
; STATE: MO
; COUNTRY: United States
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette (3.5in, 1.44 MB)
; COMPUTER: IBM PC/XT/AT, IBM PS/2 or compatibles
; OPERATING SYSTEM: Windows 95/NT
; SOFTWARE: Winzip 6.3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/089,810
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavin Jr., Lawrence M.
; REGISTRATION NUMBER: 30,768
; REFERENCE/DOCKET NUMBER: 38-21(15395)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 737-6670
; TELEFAX: (314) 737-6047
; INFORMATION FOR SEQ ID NO: 829:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Glycine max
; DEVELOPMENTAL STAGE: R3+R5 drought stressed

TISSUE TYPE: root
IMMEDIATE SOURCE:
LIBRARY: SOTMON028
CLONE: 701097624H1
US-60-089-810-829

Query Match
Best Local Similarity 70.5%; Score 161.4; DB 77; Length 305;
Matches 190; Conservative 0; Mismatches 35; Indels 2; Gaps 2;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 60
DB 38 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 96
QY 61 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAAATGCGCAAAATCTGGCACTCAATAT 120
DB 97 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAAATGCGCAAAATCTGGCACTCAATAT 155
QY 121 TCGTTGAAAAGGCTTCCCAATTCGGTTAAACAACGAAACCAATTCAGAGTTATTTGGGC 180
DB 156 TCGTTGAAAAGGCTTCCCAATTCGGTTAAACAACGAAACCAATTCAGAGTTATTTGGGC 215
QY 181 CATAAGACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 227
DB 216 NNGAGAACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 262

RESULT 10
US-09-300-482-70
Sequence 70, Application US/09300482
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Pesche, Virginia M.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
FILE REFERENCE: 04983.0031.US01/38-21(15365)B
CURRENT APPLICATION NUMBER: US/09/300,482
CURRENT FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 699
SEQ ID NO 70
LENGTH: 261
TYPE: DNA
ORGANISM: Glycine max
US-09-300-482-70

Query Match
Best Local Similarity 67.2%; Score 153.8; DB 20; Length 261;
Matches 195; Conservative 0; Mismatches 32; Indels 2; Gaps 2;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 60
DB 7 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 65
QY 61 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAAATGCGCAAAATCTGGCACTCAATAT 120
DB 66 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAAATGCGCAAAATCTGGCACTCAATAT 125
QY 121 TCGTTGAAAAGGCTTCCCAATTCGGTTAAACAACGAAACCAATTCAGAGTTATTTGGGC 180
DB 126 TCGTTGAAAAGGCTTCCCAATTCGGTTAAACAACGAAACCAATTCAGAGTTATTTGGGC 184
QY 181 CATAAGACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 229
DB 185 CAGTGAACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 233

RESULT 11
US-09-304-517A-109274
Sequence 109274, Application US/09304517A
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong

TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38-21(15097)B
CURRENT APPLICATION NUMBER: US/09/304,517A
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 295529
SEQ ID NO 109274
LENGTH: 261
TYPE: DNA
ORGANISM: Glycine max
US-09-304-517A-109274

Query Match
Best Local Similarity 67.2%; Score 153.8; DB 20; Length 261;
Matches 195; Conservative 0; Mismatches 32; Indels 2; Gaps 2;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 60
DB 7 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 65
QY 61 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAAATGCGCAAAATCTGGCACTCAATAT 120
DB 66 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAAATGCGCAAAATCTGGCACTCAATAT 125
QY 121 TCGTTGAAAAGGCTTCCCAATTCGGTTAAACAACGAAACCAATTCAGAGTTATTTGGGC 180
DB 126 TCGTTGAAAAGGCTTCCCAATTCGGTTAAACAACGAAACCAATTCAGAGTTATTTGGGC 184
QY 181 CATAAGACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 229
DB 185 CAGTGAACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 233

RESULT 12
US-09-371-146A-109274
Sequence 109274, Application US/09371146A
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong
TITLE OF INVENTION: ANNOTATED PLANT GENES
FILE REFERENCE: 38-21(15097)C
CURRENT APPLICATION NUMBER: US/09/371,146A
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 09/304,517
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 294310
SEQ ID NO 109274
LENGTH: 261
TYPE: DNA
ORGANISM: Glycine max
US-09-371-146A-109274

Query Match
Best Local Similarity 67.2%; Score 153.8; DB 21; Length 261;
Matches 195; Conservative 0; Mismatches 32; Indels 2; Gaps 2;

QY 1 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 60
DB 7 CAGACCTTATTTTCTGTCATTTGCTTCAAAATTCAGAGATTAATTAATGCGCTCAACC 65
QY 61 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAAATGCGCAAAATCTGGCACTCAATAT 120
DB 66 CACAACAGAAATAGGCTTCTGCTGATTTGGCTGTTAAATGCGCAAAATCTGGCACTCAATAT 125
QY 121 TCGTTGAAAAGGCTTCCCAATTCGGTTAAACAACGAAACCAATTCAGAGTTATTTGGGC 180
DB 126 TCGTTGAAAAGGCTTCCCAATTCGGTTAAACAACGAAACCAATTCAGAGTTATTTGGGC 184
QY 181 CATAAGACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 229
DB 185 CAGTGAACGAGCAAAACAGAGAAACCTTCAATTTATGGGGAAC 233

RESULT 13

```

US-09-985-678-109274
; Sequence 109274, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Chelinh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517,255/38-11(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 109274
;
; LENGTH: 261
;
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-109274

```

Query Match	67.2%;	Score 153.8;	DB 45;	Length 261;
Best Local Similarity	85.2%;	Pred. No. 4.5e-37;		
Matches 195; Conservative	0;	Mismatches 32;	Indels 2;	Gaps 2

QY	1	CAGACCTATTTTTTCGTCATTTGGTTCAAAATTCAGAGATTAATTAATGCGCTCAACC	60
Db	7	CAGACCTATTATTTCGTGTCATTTGGTTCAAAATTCAGAGATTAATTAATGCGCTCAACC	65
QY	61	CAGACAGAGATATAGGCTTCGTGGATTTGGCTGTATATGGCCAAATTCGGCACCTCAATAT	120
Db	66	CACACAGAGATATAGGCTTCGTGGATTTGGCTGTATATGGCCAAATTCGGCACCTCAATAT	125
QY	121	TGCTTGAAGAGGCTTCCCAATTCGGGTTAACAAGAACCAATTCAGAGTTATATGGGC	180
Db	126	TGC-TGAGAAAGGCTTCCCAATTCGTGTTTAAACAAGAACCACTTCCAAGTTATATAGA	184
QY	181	CATTAAGCAGACCAACCAAGAAAGAACTTTCATTTATGGGAAACA	229
Db	185	CAGTAGACAGCAAAACAGAAAGAAATCTTCAGTTATATGGCTACCA	233

```

RESULT 14
US-09-874-708A-16025
; Sequence 16025; Application US/09874708A
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51933) B
; CURRENT APPLICATION NUMBER: US/09/874,708A
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/721,750
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 91742
; SEQ ID NO 16025
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(447)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: uC-gmwtomsoy099e0zbl
; US-09-874-708A-16025

```

Query Match	67.2%;	Score 153.8;	DB 37;	Length 447;
Best Local Similarity	85.2%;	Pred. No. 5.6e-37;		
Matches 195; Conservative	0;	Mismatches 32.	Indels 3.	Cans 3.

Qy 1 CAGACCTTATTTTCTGTCAATTGCTTCAAATTTGAGAGATTATTAATGCGCTCAACC 60
Ddb 23 CAGACCTTATTTTCTGTCAATTGCTTCAAATTTGAGAGATTATTAATG-GCTCAACC 81

Qy 6 CAAACAAGAAATATGGCTTCGTGATTTGGCGTTAAATGGCCAAATATGGCACTCAATAT 120
Db 82 CACAAACAAATATGGCTTCGTGATTTGGCGTTAAATGGCCAAATATCGGAGCTCAATAT 141
Qy 121 TCGTTGAAAAGGCGTCCCAATTCGCGTTAAACAAAGCAACCATTTCCAGGTTATTTGGGC 180
Db 142 TGC-TGAGAAAGCTTTCCCATTTCTGTATTCAACCGAACCACTCCAAAGTTGATGAGA 200
Qy 181 CATAGACGAGCAAAACGAGAGGAAACCTTCAATTATTTGGGACAA 229
Db 201 CAGTACAAAGCAAAACAGAGGAAATCTTCCAGTTATTTGGCTACA 249

```

RESULT 15
US-60-211-750-15882
; Sequence 15882, Application US/60211750
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51933)A
; CURRENT APPLICATION NUMBER: US/60/211,750
; CURRENT FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 90609
; SEQ ID NO 15882
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: uc-gmrom1nseq039e02b1
; US-60-211-750-15882

```

Query Match	67.2%;	Score 153.8;	DB 90;	Length 447;
Best Local Similarity	85.2%;	Pred. No. 5.6e-37;		
Matches 195;	Conservative 0;	Mismatches 32;	Indels 2;	Gaps 2

QY	1	CAGACCTTATTTTCTGCAATTTGCTCCAAATTGAGAGATTAAATTATGCGCTCAAC	60
Db	23	CAGACCTTATTTTCTGCAATTTGCTCCAAATTGAGAGATTAAATTATG-GCTCAAC	81
QY	61	CACAAACAAGATAGGCGCTTGCTGATTTGGCTGTTAATGGGCAAAATCGGCACCTCAT	120
Db	82	CACAAACAAGATAGGCGCTTGCTGATTTGGCTGTTAATGGGCAAAATCTGGCAGCTCAAT	141
QY	121	TGCTTGAAAAGGGCTTCCCAATTCGGTTAAACAAGAACATTTCAGGTTATTGGGC	180
Db	142	TGC-TGAGAAAGGCTTCCCAATTTCTGTTTCAACGCAACACTTCCAGGTTGATGAGA	200
QY	181	CATTAGACGAGCAAAACGAGAGGAAACCTTCAATTTATGGGAGACAA	229
Db	201	CAGTGAACAGGCAAAACMAAGGAATCTTCCAGTTATGGCTACCA	249

Search completed: May 4, 2005, 20:13:31
Job time : 1836.74 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 92.4677 Seconds
(without alignments)
5591.850 Million cell updates/sec

Title: US-09-300-482-225

Perfect score: 316

Sequence: 1 gataagcgccgacactgaggtgagggaggtactcga 316

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/6C.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54.8	17.3	907	US-09-620-312D-617	Sequence 617, App
2	54.8	17.3	961	US-09-620-312D-618	Sequence 618, App
3	51.8	16.4	795	US-09-248-796A-3134	Sequence 3134, Ap
4	50.4	15.9	271	US-09-313-294A-3583	Sequence 3583, Ap
5	46.2	14.6	1246	US-09-691-270A-19	Sequence 19, Appl
6	38	12.0	663	US-09-107-532A-2422	Sequence 2422, Ap
7	34.4	10.9	395	US-09-404-879A-378	Sequence 378, App
8	34.4	10.9	395	US-09-667-857-378	Sequence 378, App
9	34.4	10.9	591	US-09-854-133-314	Sequence 314, App
10	34.4	10.9	601	US-09-949-016-22949	Sequence 22949, A
11	34.4	10.9	601	US-09-949-016-22950	Sequence 22950, A
12	34.4	10.9	601	US-09-949-016-22951	Sequence 22951, A
13	34.4	10.9	601	US-09-949-016-195227	Sequence 195227,
14	34.4	10.9	601	US-09-949-016-195228	Sequence 195228,
15	34.4	10.9	601	US-09-949-016-195229	Sequence 195229,
16	34.4	10.9	613	US-09-328-111-389	Sequence 389, App
17	34.4	10.9	667	US-09-328-111-388	Sequence 388, App
18	34.4	10.9	810	US-09-404-879A-206	Sequence 206, App
19	34.4	10.9	810	US-09-318-933-206	Sequence 206, App
20	34.4	10.9	810	US-09-215-681-206	Sequence 206, App
21	34.4	10.9	810	US-09-216-003A-206	Sequence 206, App
22	34.4	10.9	810	US-09-667-857-206	Sequence 206, App
23	34.4	10.9	818	US-09-949-016-5538	Sequence 5538, Ap
24	34.4	10.9	826	US-09-949-016-239	Sequence 239, App
25	34.4	10.9	1482	US-09-566-921-93	Sequence 93, Appl
26	34.4	10.9	7495	US-09-949-016-11981	Sequence 11981, A
27	34.4	10.9	7496	US-09-949-016-11280	Sequence 11280, A

C	28	34	10.8	3693	3	US-09-056-226-1	Sequence 1, Appl
	29	33.8	10.7	3639	2	US-08-737-524B-26	Sequence 26, Appl
	30	33.8	10.7	4315	4	US-09-444-905-1	Sequence 1, Appl
	31	33.4	10.6	702	4	US-09-328-352-1855	Sequence 1855, Ap
	32	33.4	10.6	263693	4	US-09-949-016-12386	Sequence 12386, A
	33	33.4	10.6	263694	4	US-09-949-016-12386	Sequence 12386, A
	34	33.2	10.5	4315	4	US-09-444-905-1	Sequence 1, Appl
	35	33	10.4	42574	4	US-09-949-016-17525	Sequence 17525, A
	36	32.8	10.4	1149	3	US-09-257-583-4	Sequence 4, Appl
	37	32.2	10.2	163022	4	US-09-949-016-16515	Sequence 16515, A
	38	32	10.1	500	4	US-09-050-739-67	Sequence 67, Appl
	39	32	10.1	1998	4	US-09-894-844-6	Sequence 6, Appl
	40	32	10.1	2050	4	US-09-050-739-69	Sequence 69, Appl
	41	32	10.1	2999	4	US-09-710-279-3482	Sequence 3482, Ap
	42	32	10.1	16885	1	US-08-390-878-16	Sequence 16, Appl
	43	32	10.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl
	44	32	10.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl
	45	31.8	10.1	601	4	US-09-949-001-760	Sequence 760, App

ALIGNMENTS

RESULT 1
US-09-620-312D-617
Sequence 617, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 617
LENGTH: 907
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (61)..(747)
US-09-620-312D-617

Query Match 17.3% Score 54.8; DB 4; Length 907;
Best Local Similarity 50.0%; Pred. No. 5.6e-09;
Matches 137; Conservative 0; Mismatches 137; Indels 0; Gaps 0;
DB 4 AAGTGCACACACTGAGAAAGATACCTTCCTTGACATAGAGTTGATGTTGCTA 63
595 AAGTGCACCTGTTAGAGACCAAGTTCCATCTTGGATATAGAGTGCATGAGTGA 594

OY 6 GGTCTTCAACCAATAGACGTGGCCGATCTGCTGGGGCCAAATTCAGTGTGCTGAAGC 123
 |||||
 Db 595 GGTCTTCAACCACTGTCCATTAATATGTGACAGGACGAGCTTAACATATGATTTGTCTGGCAGT 654
 |||||
 OY 124 TCTAATATTTGGCGCTCGGACCCAGAGGCATATATCTGCTGAGGAAGAAGCGTGCAG 183
 |||||
 Db 655 GCTATTATGAGGAGTAAAGACCCGCAATCTTGATCAATCTATTATTAAGAAAGTTTGGTCA 714
 |||||
 OY 184 GGCTTTCAGAACAAAACCTGATTTTGGTGTCTCTGTAAAGTACTCCCTCGTTTTT 243
 |||||
 Db 715 GAAGCTGCTCAGAAAGTTCTCTGTGATCGGTAAACATTAAGAGCCACGATGTTCCGTT 774
 |||||
 OY 244 TTATTGTCGCGTTTGTAGTCAAAACATAACTA 277
 |||||
 Db 775 CATGAATCTCCCTTTTACTGGAAAAACGGAATA 808
 |||||

```

US-09-620-312D-618
; Sequence 618, Application US/09620312D
; Patent No. 6559662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aihong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6559662el Nucleic Acids and
; FILE REFERENCE: 784C1P2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ. ID NOS: 1105
; SOFTWARE: pt_fl_genes Version 1.0
; SEQ ID NO 618
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(801)
; US-09-620-312D-618

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Query Match	17.3%	Score 54.8;	DB 4;	Length 961;
Best Local Similarity	50.0%;	Pred. No. 5.8e-09;		
Matches 137;	Conservative 0;	Mismatches 137;	Indels 0;	Gaps 0;
QY	4	AGGGTGGGCACACGTAGAGAAAGATGACCCCTTCCCTTGCACATAGAGGTTGATGCTGTCTA	63	
Db	589	AGGGTTACTGCTGGTTGAGAGCCAGCTCCCATCTTTGGATATAGAGGTGATGCTGAGCTA	648	
QY	64	GGTCCCTCAACCATATAGCGTGGCCGACATCTGTGGGCGCAATTCATGCTGCTGGGAAGC	123	
Db	649	GGTCCCTCACTGTCATTAATATGTCGAGAGGACAGAGCTAATCATGATGTGCTGGCGAGT	708	
QY	124	TCTATATTTGGCGCTGGGAGCCGAGAGCCATCATATCTGTGCTGAGGAAGAAGCTGCAG	183	

Db	709	GCATTATATAGAGATGAGAACCCAGCATCTGATCAATCTATTAAAGAAATGTTTCTCA	768
Qy	184	GGCTCTCAGAAAGAAAAACGATTTTGGTGTTTCTGCTGTAAAGTACTCCCTCGGTTTTT	243
Db	769	GAAGCTGCTCAGAAAGCGTTCTTGATCGGGAAACCATTAAGAGCCAGTGTCTCGTT	828
Qy	244	TTTATTGTCGGGTTTATGTTCAACATGAACCTA	277
Db	829	CATGAATCTCCCTTTTACTGGAAACAGGATA	862

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RESULT 3
US-09-248-796A-3134
; Sequence 3134, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Kelch weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 3134
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Candida albicans
; IS-09-248-796A-3134

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Query Match	Similarity	Score	DB 4	Length
Best Local	60.18	Pred. No. 6.1e-08		795
Matches	86	Conservative	0	Matches 57; Indels 0; Gaps 0;
QY	4	AAGGTGGCACACATGAGAAAGAAAGTACCCCTTCCTTGACATAGAGGTTGATGGTGTCTA	63	
Db	589	AAGGTCAAAACATTAAAGAAAAATTAACCCCAACTTGTGATGTTCAAGTTGATGGAGGATTG	648	
QY	64	GGTCTTCAACCATAGACGTGGCCGCATCTGCTGGGGCAATTGCATGTCGTGAAGC	123	
Db	649	GGGAAGGATCAATTCAACCTGTGCAGATGTGTGCATATGATGTGTGCTGGAGCC	708	
QY	124	TCTAATTTGGCGGTGGGACC	146	
Db	709	TCCGTGTTTAAACGAGAGACC	731	

```

RESULT 4
US-09-313-294A-3583/C
/ Sequence 3583, Application US/09313294A
/ Patent No. 6476212
/ GENERAL INFORMATION:
/ APPLICANT: Lalgudi, Raghunath V.
/ APPLICANT: Ito, Laura Y.
/ APPLICANT: Sherman, Bradley K.
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
/ FILE REFERENCE: PI-0017 US
/ CURRENT APPLICATION NUMBER: US/09/313,294A
/ CURRENT FILING DATE: 1999-05-14
/ NUMBER OF SEQ ID NOS: 7600
/ SOFTWARE: PERL Program
/ SEQ ID NO 3583
/ LENGTH: 271
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: Incyte ID No. 6476212 700611933H1
/ NAME/KEY: unsure
/ LOCATION: 244, 259

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OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3583

Query Match 15.9%; Score 50.4; DB 4; Length 271;
Best Local Similarity 78.9%; Pred. No. 1.1e-07;
Matches 71; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 224 AGTACTCCCTCGCTTTTATTCGCGCTTTAGTCAACATGACTAGCGGAC 283
DB 269 AATATATCCNCATCTTTTATNTGCGGCTTTAGTTGAA-ATGAACTAGCGGAC 211
QY 284 GACTGATTCGAGATGAGGAGACTT 313
DB 210 GCGAAATTCGAGACAGATGACTT 181

RESULT 5

US-09-691-270A-19/c
Sequence 19, Application US/09691270A

Patent No. 662795
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Sean J. Coughlan
TITLE OF INVENTION: CAROTENOID BIOSYNTHESIS ENZYMES
FILE REFERENCE: B1115 US NA2
CURRENT APPLICATION NUMBER: US/09/691,270A
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: 60/083,042
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: PCT/US99/08789
PRIOR FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: MICROSOFT OFFICE 97
SEQ ID NO 19
LENGTH: 1246
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (367)
OTHER INFORMATION: n = a, c, g or t
US-09-691-270A-19

Query Match 14.6%; Score 46.2; DB 4; Length 1246;
Best Local Similarity 76.0%; Pred. No. 7.9e-06;
Matches 57; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 240 TTTTATTCGCGCTTTAGTCAACATGACTAGCGGACTGATATTCGAGAA 299
DB 1104 TTTTATTCGCGCTTTAGTCAACATGACTAGCGGACTGATATTCGAGAA 1045
QY 300 TCGAGGAGTACTC 314
DB 1044 CGAGTGTATCTTTC 1030

RESULT 6

US-09-107-532A-2422
Sequence 2422, Application US/09107532A

Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2422:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...663

SEQUENCE DESCRIPTION: SEQ ID NO: 2422:
US-09-107-532A-2422

Query Match 12.0%; Score 38; DB 4; Length 663;
Best Local Similarity 55.2%; Pred. No. 0.0047;
Matches 74; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 15 ACTGAGAAAGAGTACCTTCCCTTGACATGAGGTGATGCTGCTTCAC 74
DB 492 ACTGAGAGAAACAATTGACTTATGCATCGAAGTAGTGCGGAAATCTCCAGAAAC 551
QY 75 CATGACGTGGCGGATCTGTCGGCCAAATGCAATGCTGCTGAAGCTTAATTTGG 134
DB 552 AGCAAAATCTGTAAGATGACGGGCGGATGCTTCTGTCAGATCATATATCTATG 611
QY 135 CGCTGGGACCCAG 148
DB 612 AGCCGAAATCCAG 625

RESULT 7

US-09-404-879A-378/c
Sequence 378, Application US/09404879A

Patent No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 378
LENGTH: 395
TYPE: DNA
ORGANISM: Homo sapiens

US-09-404-879A-378

Query Match 10.9%; Score 34.4; DB 3; Length 395;
Best Local Similarity 63.1%; Pred. No. 0.068;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGCTAGGTCCTTCAACCATAGACGTGGCCGATCTGCTGGGCCAATTGCATGCTGC 116
DB 109 TGGTGCAGGTGCTGCAACAGTAGAGTGGCTGTTGCTGCTGATTGGAAACAGTCTT 50

QY 117 TGGAGCTTATATTGGCGCTGC 140
DB 49 TGGCAGCCTTATCATTTGATATGC 26

RESULT 8

US-09-667-857-378/c
Sequence 378, Application US/09667857
Patent No. 6699664
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Reiter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C5
CURRENT APPLICATION NUMBER: US/09/667,857
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 378
LENGTH: 395
TYPE: DNA
ORGANISM: Homo sapiens
US-09-667-857-378

Query Match 10.9%; Score 34.4; DB 4; Length 395;
Best Local Similarity 63.1%; Pred. No. 0.068;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGCTAGGTCCTTCAACCATAGACGTGGCCGATCTGCTGGGCCAATTGCATGCTGC 116
DB 109 TGGTGCAGGTGCTGCAACAGTAGAGTGGCTGTTGCTGCTGATTGGAAACAGTCTT 50

QY 117 TGGAGCTTATATTGGCGCTGC 140
DB 49 TGGCAGCCTTATCATTTGATATGC 26

RESULT 9

US-09-854-133-314
Sequence 314, Application US/09854133
Patent No. 6759508
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Radoch
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 314
LENGTH: 591

TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(591)
OTHER INFORMATION: n = A,T,C or G
US-09-854-133-314

Query Match 10.9%; Score 34.4; DB 4; Length 591;
Best Local Similarity 63.1%; Pred. No. 0.086;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGCTAGGTCCTTCAACCATAGACGTGGCCGATCTGCTGGGCCAATTGCATGCTGC 116
DB 328 TGGTGCAGGTGCTGCAACAGTAGAGTGGCTGTTGCTGCTGATTGGAAACAGTCTT 387

QY 117 TGGAGCTTATATTGGCGCTGC 140
DB 388 TGGCAGCCTTATCATTTGATATGC 411

RESULT 10

US-09-949-016-22949/c
Sequence 22949, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22949
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-22949

Query Match 10.9%; Score 34.4; DB 4; Length 601;
Best Local Similarity 63.1%; Pred. No. 0.086;
Matches 53; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGCTAGGTCCTTCAACCATAGACGTGGCCGATCTGCTGGGCCAATTGCATGCTGC 116
DB 164 TGGTGCAGGTGCTGCAACAGTAGAGTGGCTGTTGCTGCTGATTGGAAACAGTCTT 105

QY 117 TGGAGCTTATATTGGCGCTGC 140
DB 104 TGGCAGCCTTATCATTTGATATGC 81

RESULT 11

US-09-949-016-22950/c
Sequence 22950, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768

;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO: 22950
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-22950

Query Match
Best Local Similarity 10.9%; Score 34.4; DB 4; Length 601;
Matches 53; Conservativity 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGTCTAGGCTCTTAACCATAGAGTGGCGCCATCTGCTGGGGCCAAATTGCGTGGC 116
DB 266 TGGTCAAGGTGCTGCAACAGTAGAGTGGCTGTTCTGTGCTGGTATTGGAACAGTCTT 207
QY 117 TGGAGCTCTATATTGGCGCTGC 140
DB 206 TGGCAGCCTTATCATTTGTTATGC 183

RESULT 12
US-09-949-016-22951/c
; Sequence 22951, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 22951
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-22951

US-09-949-016-22951

Query Match
Best Local Similarity 10.9%; Score 34.4; DB 4; Length 601;
Matches 53; Conservativity 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGTCTAGGCTCTTAACCATAGAGTGGCGCCATCTGCTGGGGCCAAATTGCGTGGC 116
DB 554 TGGTCAAGGTGCTGCAACAGTAGAGTGGCTGTTCTGTGCTGGTATTGGAACAGTCTT 495
QY 117 TGGAGCTCTATATTGGCGCTGC 140
DB 494 TGGCAGCCTTATCATTTGTTATGC 471

RESULT 13
US-09-949-016-195227/c
; Sequence 195227, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO: 195227
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-195227

Query Match
Best Local Similarity 10.9%; Score 34.4; DB 4; Length 601;
Matches 53; Conservativity 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGTCTAGGCTCTTAACCATAGAGTGGCGCCATCTGCTGGGGCCAAATTGCGTGGC 116
DB 164 TGGTCAAGGTGCTGCAACAGTAGAGTGGCTGTTCTGTGCTGGTATTGGAACAGTCTT 105
QY 117 TGGAGCTCTATATTGGCGCTGC 140
DB 104 TGGCAGCCTTATCATTTGTTATGC 81

RESULT 14
US-09-949-016-195228/c
; Sequence 195228, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 195228
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-195228

Query Match
Best Local Similarity 10.9%; Score 34.4; DB 4; Length 601;
Matches 53; Conservativity 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 TGGTCTAGGCTCTTAACCATAGAGTGGCGCCATCTGCTGGGGCCAAATTGCGTGGC 116
DB 266 TGGTCAAGGTGCTGCAACAGTAGAGTGGCTGTTCTGTGCTGGTATTGGAACAGTCTT 207
QY 117 TGGAGCTCTATATTGGCGCTGC 140
DB 206 TGGCAGCCTTATCATTTGTTATGC 183

RESULT 15
US-09-949-016-195229/c
; Sequence 195229, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 ; Search time 113.536 Seconds
(without alignments)
5591.830 Million cell updates/sec

Title: US-09-300-482-298

Perfect score: 388
Sequence: 1 ggagagaagaagaagaatg.....ttaagctgggagcccccgt 388

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155.2	40.0	267	4	US-09-313-294A-2427
2	88.8	22.9	907	4	US-09-620-312D-617
3	88.8	22.9	3556	3	US-09-276-531-8
4	85	21.9	961	4	US-09-620-312D-618
5	83.6	21.5	916	4	US-08-956-171E-1149
6	83.6	21.5	916	4	US-08-781-986A-1149
7	80.8	20.8	903	4	US-09-583-110-947
8	80.8	20.8	993	4	US-09-107-433-453
9	79.4	20.5	663	4	US-09-107-532A-2422
10	77.8	20.1	690	4	US-09-134-000C-1299
11	77.6	20.0	12566	3	US-08-961-527-149
12	76.4	19.7	1230025	4	US-09-198-452A-1
13	76.4	19.7	1230230	4	US-09-513-999C-1817
14	75.8	19.5	434	4	US-09-902-540-9495
15	75.6	19.5	643	4	US-09-902-540-9495
16	75.6	19.5	14101	4	US-09-902-540-1080
17	69	11.8	493	3	US-09-221-017B-1557
18	68.2	11.6	723	4	US-09-543-681A-2557
19	68	17.5	560	4	US-09-710-279-3071
20	68	17.5	645	3	US-09-134-001C-1986
21	68	17.5	672	4	US-09-710-279-3077
22	68	17.5	3008	4	US-09-710-279-3513
23	68	17.5	3246	4	US-09-710-279-4257
24	68	17.5	3276	4	US-09-710-279-4240
25	67	17.3	795	4	US-09-248-796A-3134
26	65.4	16.9	1234	3	US-08-858-207A-110
27	60.6	15.6	4403765	3	US-09-103-840A-2

28	60.6	15.6	441529	3	US-09-103-840A-1	Sequence 1, Appli
C 29	58	14.9	1019	3	US-08-714-918-79	Sequence 79, Appl
C 30	58	14.9	1019	3	US-09-265-315-79	Sequence 79, Appl
C 31	58	14.9	1019	3	US-09-265-315-79	Sequence 79, Appl
C 32	58	14.9	1019	3	US-09-266-417-79	Sequence 79, Appl
C 33	58	14.9	1019	4	US-09-528-709-79	Sequence 79, Appl
C 34	58	14.9	1019	4	US-09-527-745-79	Sequence 79, Appl
C 35	56	14.4	705	4	US-09-489-039A-2344	Sequence 2344, Ap
C 36	54.4	14.0	702	4	US-09-328-352-1855	Sequence 1855, Ap
C 37	52.8	13.6	1830121	4	US-09-557-884-1	Sequence 1, Appli
C 38	52.8	13.6	1830121	4	US-09-643-990A-1	Sequence 1, Appli
C 39	51.8	13.4	410	4	US-09-513-999C-1816	Sequence 1816, Ap
C 40	51.4	13.2	1664976	4	US-08-916-421B-1	Sequence 1, Appli
C 41	51.4	13.2	1664976	4	US-09-592-002-31	Sequence 31, Appl
C 42	48.8	12.6	65792	4	US-09-790-988-1	Sequence 1, Appli
C 43	47	12.1	640681	4	US-09-252-991A-825	Sequence 825, App
C 44	46	11.9	693	4	US-09-489-039A-2525	Sequence 2525, Ap
C 45	42.2	10.9	696	4	US-09-489-039A-2525	Sequence 2525, Ap

ALIGNMENTS

RESULT 1
US-09-313-294A-2427
Sequence 2427, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Ialqudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 2427
LENGTH: 267
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700552657H1
US-09-313-294A-2427

Query Match 40.0%; Score 155.2; DB 4; Length 267;
Best Local Similarity 75.4%; Pred. No. 1.5e-42;
Matches 193; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY	116	GCTCCATGACATGATGATGGGCAATTTGTCCTCAATTTACTATTGGGCTCCACT	175
DB	1	GCTACATATGACATGATGATGGGCACTGCTCTCACTGATGATGATGGGCTCCGCT	60
QY	176	TATTGAAGTTGAGAAAGCACAAAGCATTTTGGATTTGCTACCTTATGTTACAA	235
DB	61	GATTCAGAGCTTGAGAAACATACCAAGCATTTTGGATGCTGCTATATGTCACAA	120
QY	236	TCCCTTGATTTATGTTGAACCTTGCAAAAGCTGGTCTGCTTTTACATTTACAGT	295
DB	121	GCTTCAATTTACGTAAGCACTTTGGAAGGCTGCGCTTCTGATTCACATTTCAAT	180
QY	296	AGAGACATCAAAAGTAATCTGGAAGAACTTATCCAAAGATCAAGTCAATGATGAT	355
DB	181	AGAACTGCTGAGACAACTGGCAAGATCTATCCAAAGATTAATCAAAAGGTATGCG	240
QY	356	TCTTGCTGATGATTA 371	
DB	241	GCTGTGATATCATGA 256	

RESULT 2
US-09-620-312D-617

/ Sequence 617, Application US/09620312D
/ Patent No. 6569662
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Xue, Aiding J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yundong
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinghast
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 6569662el Nucleic Acids and
/ FILE REFERENCE: Polypeptides
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1105
/ SOFTWARE: PC_FL_genes Version 1.0
/ SEQ ID NO 617
/ LENGTH: 907
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (61)..(747)
/ US-09-620-312D-617

Query Match 22.9%; Score 88.8; DB 4; Length 907;
Best Local Similarity 56.9%; Pred. No. 1,2e-19;
Matches 206; Conservative 0; Mismatches 147; Indels 9; Gaps 2;
QY 33 AAAATAGCTCTTCGATGCTCTTCGACCTTCGCAATTTGGCTTCGAGGCTGAGGC 92
Db 76 AAGATTGGCCGCTCATCTCAACAGCAGCTGGCCATTAGGGGCCGAGTCTCCGG 135
QY 93 ATGCTCCACTTGGGCGCGATTTGCTCCACATGACATCATGATGGGCAATTTGTCCC 152
Db 136 ATGCTAGACTTGGGCGCGATTTATCTGACCTGAGCCTAATGAGCGGCAATTTGTCCC 195
QY 153 AATTAACTAATTTGGGCTCCAGTATTTGAAGTTGAAGAAAGCA-----CACAAAGCA 206
Db 196 AACATCACCTTTGGTACCTCTGTGTAGAAAGCTTCGAAAGCGTAGGCGCAGACCT 255
QY 207 TATTGGATTGTACCTTATGTTAAATCCTCTTGAATTAATTTGAACCTTTGCCAAA 266
Db 256 TTTCTTTGACATGACATGATGTGTCCAAAGCAGAAAGTGGGTAAAGCCATAGCTGTA 315
QY 267 GCTGTGCTTGGTGTATTACATTTACAGTACATGACATCAAAAGATTAAGTGAAGAACTT 326
Db 316 GCAAGAGCAATCACTAGTACACCTTTATCTCGAG--GCTACTGAGAACCCAGGGGCTTTTG 372
QY 327 ATCCAAAGAAATCAAGTACATGACATGATGCTGTGGTGTAGCATTAAGCCGAGGACCC 386
Db 373 ATTAAGACATTCGGAGAAATGGGATGAAGTTGGCTTCGATCAACAGAAAGCACTCA 432
QY 387 GT 388
Db 433 GT 434

RESULT 3
US-09-276-531-8
/ Sequence 8, Application US/09276531
/ Patent No. 618968
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Lal, Preeti
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Yue, Henry
/ APPLICANT: Reddy, Roopa
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Baughn, Mariah R.
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
/ NUMBER OF SEQUENCES: 134
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 FORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/276,531
/ FILING DATE: Herewith
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/079,677
/ FILING DATE: March 27, 1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lynn E. Murry, Ph.D.
/ REGISTRATION NUMBER: 42,918
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3556 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: L1VTTUT01
/ CLONE: 1753826
/ US-09-276-531-8
Query Match 22.9%; Score 88.8; DB 3; Length 3556;
Best Local Similarity 56.9%; Pred. No. 2.7e-19;
Matches 206; Conservative 0; Mismatches 147; Indels 9; Gaps 2;
QY 33 AAAATAGCTCTTCGATGCTCTTCGACCTTCGCAATTTGGCTTCGAGGCTGAGGC 92
Db 72 AAGATTGGCCGCTCATCTCAACAGCAGCCTGGCCATTAGGGGCCGAGTCTCCGG 131
QY 93 ATGCTCCACTTGGGCGCGATTTGCTCCACATGACATCATGATGGGCAATTTGTCCC 152
Db 132 ATGCTAGACTTGGGCGCGATTTATCTGACCTGAGCCTAATGAGCGGCAATTTGTCCC 191
QY 153 AATTAACTAATTTGGGCTCCAGTATTTGAAGTTGAAGAAAGCA-----CACAAAGCA 206
Db 192 AACATCACCTTTGTGACCTGTGTAGAAAGCTTCGAAAGAGTGAAGCCAGGACCT 251
QY 207 TATTGGATTGTACCTTATGTTAAATCCTCTTGAATTAATTTGAACCTTTGCCAAA 266
Db 252 TTTCTTTGACATGACATGATGTGTCCAAAGCAGAAAGTGGGTAAAGCCATAGCTGTA 311

QY 267 GCTGTCCTTCTGTTTACATTCAGTACATCAAGATACATGAAAGACTT 326
 DB 312 GAGGAGCCAAATCAGTACACCTTCTCTGAG--GCTACTGAGAACCCAGGGCTTTG 368
 QY 327 ATCCAAAGATCAAGTACATGATGATTCCTGTGTAGCATTTAAAGCTTGGACCC 386
 DB 369 ATTTAAAGACATTCGGAGATGAGATGAGATGAGTGGCTTCCATCAACACGAGAACTTA 428

QY 387 GT 388
 DB 429 GT 430

RESULT 4
 US-09-620-312D-618
 ; Sequence 618, Application US/09620312D
 ; Patent No. 6569662
 ; GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
 APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyen
 APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
 APPLICANT: Xue, Aildong J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yundong
 APPLICANT: Wang, Duntui
 APPLICANT: Wang, Zhiwei
 APPLICANT: John Tillinghast
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. 656962e1 Nucleic Acids and
 TITLE OF INVENTION: Polypeptides
 FILE REFERENCE: 784CIP2B
 CURRENT APPLICATION NUMBER: US/09/620,312D
 FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1105
 SOFTWARE: pt_FL_genes Version 1.0
 SEQ ID NO 618
 LENGTH: 961
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (61)..(801)
 US-09-620-312D-618

Query Match 21.9%; Score 85; DB 4; Length 961;
 Best Local Similarity 59.6%; Pred. No. 2.4e-18;
 Matches 164; Conservative 0; Mismatches 105; Indels 6; Gaps 1;

QY 33 AAAATAGCTCTTCATGCTCTCTCCGACTTCGCCAATTTGGCTTCGAGGCTACGCC 92
 DB 76 AAGATTGGCCGCTCACTCTCAACAGACCTGGCCAAATTTAGGGGCGAGTCCCTCCG 135
 QY 93 ATGCTCCACTTCGCGCCGATGCTCCACATGACATGATGGGATTTTGTCC 152
 DB 136 ATGCTAGACTCTGGGCGCATATCTGCACCTGAGATGAGACGGGATTTTGTCC 195
 QY 153 AATTACTATTGGCGCTCCAGTTATTTGAAGTGAAGCA-----CACAAAGCA 206
 DB 196 AACATCACCTTGGTCACTGCTGAGAAAGCTTCGAAAGAGCTAGGCGAGACCTT 255
 QY 207 TATTGGATTCACCTTATGTTAAATCTCTGATTATGTTAAACCTTGGCAAA 266

DB 256 TTCTTGACATGACATGATGTGTCCAAGACCAAGATGGGTAAGCAATGCTGTA 315
 QY 267 GCTGTCCTTCTGTTTACATTTACAGTAGAC 301
 DB 316 GCAGAGCCAAATCAGTACACCTTCTCATCTCGAGC 350

RESULT 5
 US-08-956-171E-1149/C
 ; Sequence 1149, Application US/08956171E
 ; Patent No. 6593114
 ; GENERAL INFORMATION:
 APPLICANT: Charles Kunach
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5256
 CORRESPONDENCE ADDRESS:
 ADDRESS: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/956,171E
 FILING DATE: 20-Oct-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/009,861
 FILING DATE: January 5, 1996
 APPLICATION NUMBER: 08/791,986
 FILING DATE: January 3, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mark J. Hyman
 REGISTRATION NUMBER: 46,789
 REFERENCE/DOCKET NUMBER: PB248P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (240) 314-1224
 TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 1149:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 916 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 1149:
 US-08-956-171E-1149

Query Match 21.5%; Score 83.6; DB 4; Length 916;
 Best Local Similarity 53.6%; Pred. No. 7.1e-18;
 Matches 192; Conservative 2; Mismatches 161; Indels 3; Gaps 1;

QY 31 CCAAAATAGCTCTTCGATGCTCTCTCCGACTTCGCCAATTTGGCTTCGAGGCTCAGC 90
 DB 745 CAAATCTATTCATCATATTAATATCTGTGATTTTGGATTACAAACATTAATAAC 686
 QY 91 GATGCTCAGCTTCGCGCCGATGCTCCACATGACATCATGATGGGATTTTGTCC 150
 DB 685 GACTTGAAGACAGCGCGTCAAGGATTCATTTGATGATGATGATGATGATGATGATG 626
 QY 151 CCAATTTACTTTGGCGCTCCAGTTATTTGAAGTGAAGCAACAAAGGATATT 210
 DB 625 CTAATATATATTTGTTTACCAATATTAGATGACGTAAGAAAGCAACATTAACCTA 566

NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 453:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...993
SEQUENCE DESCRIPTION: SEQ ID NO: 453:
US-09-107-433-453
Query Match 20.8%; Score 80.8; DB 4; Length 993;
Best Local Similarity 53.7%; Pred. No. 6.7e-17;
Matches 191; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

33 AAAATAGCTCTTCGATGCTCTTCCTCCGACCTTCGCAATTTGGCTTCGAGGCTGAGCGC 92
349 AAGATTGCTCCGTCATCTTCGAGCAGATATGCGCACTTGAACGTGAATCAAAAGT 408
93 ATGCTCCACTTGGGGCCGATGGCTCCCATGACATATGATGGGATTTTGTCCCC 152
409 CTAGAAGCAACTGGGCGCAATATGCGCATATGATATGACAGTATTTTGAACG 468
153 AATTTAACTATTGGCGCTCCAGTTATTTGAAGTTGAGAAAGCAACAAGCATATTG 212
469 CAATACAGTTTGGTGCAGTGTGTGCGAGAGCTTCGTCCTATATGTAAGATGTTTC 528
213 GATGTCACTTATGATGTTCAAAATCTCTTGAATATGTTGAACCTTGGCAAAAGCTGT 272
529 GATTCACATCTGATGTGTTCAAACTGAGCATCATCTGGAAGATTTTGGCGGTGAGGT 588
273 GCTTCGTTTACATTTACGTTAGAGATCAAAAGATTAATCTGGAAGAAATTAATCA 332
589 GAGACATCATATGATATGATGAG--AGCAACCTCATATTCATGCGCGCTCCAA 645
333 AGAATCAAGTCAATGAGCATGATTTCTGGTGTAGCATTAAGCTGGAGCCCCGT 388
646 AAAATTCGTTCACTCGAGTAAAGCTTCAATGCTTATCATCTGACACACCAAGT 701

RESULT 9
US-09-107-532A-2422
Sequence 2422, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2422:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...663
SEQUENCE DESCRIPTION: SEQ ID NO: 2422:
US-09-107-532A-2422
Query Match 20.5%; Score 79.4; DB 4; Length 663;
Best Local Similarity 52.8%; Pred. No. 1.6e-16;
Matches 195; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

20 GGAATGACACGGAATATGATGCTCTTCGATGCTCTTCGCACTTGGCAATTTGGCTTC 79
3 GGAATGACAGATGATGATGACATTCATTTTGTAGTGCAGATTTTGGCAATTTTCAAG 62
80 CGAGGCTCAGCGCATGCTTCACCTTCGCGCGCGATTTGGCTCCATGACATGATCATGATG 139
63 AGACATGATGATGATGAGAAAAGGAGGCGAGATTAATCCAGTATGATGATGATG 122
140 GCATTTTGTCCCATTTAATATTTGGCGCTCCAGTATTTGAAGTTGAGAAAGACAC 199
123 CCAATTTTGTCCCAATATCAATTTAGGCGCAATATTTGTTAGGCAATTCGCTGTTAC 182
200 AAGGATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 259
183 TAAATTCAGTTAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 242

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QY 260 GGCAGAAAGTGTGCTCTGCTTTTACATTTCACGTAGAGACATCAAAAGATAACTGGAA 319
DB 243 TGCAGAAAGTGTGAGAGATATCATCTACGTCCACCTCCAGCAACTCTCTCATATTCATCG 302
QY 320 AGAAGCTTATCCAAAGATCAAGTACATGAGCATGATTCCTGCTGTAGATTAAGCCTGG 379
DB 303 GGCACTT---CAATGACAAAAGCTTAGAGATTAAAGCTGGAGTAGTATCAATCCAGG 359
QY 380 GACCCCGCT 388
DB 360 AACACCACT 368
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RESULT 10

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US-09-134-000C-1299
; Sequence 1299, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucelte-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1299
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1299
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Query Match 20.1%; Score 77.8; DB 4; Length 690;
Best Local Similarity 52.3%; Pred. No. 5.7e-16;

Matches 197; Conservative 0; Mismatches 177; Indels 3; Gaps 1;

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QY 9 AAGAAAGATGGGAATGACACCGAAATAGCTCTTCGATGCTCTTCGACTTCGGC 68
DB 16 AATATTAAGGAGCGAGCCAAATGAACTAGACCACTTATTAAGTCCGATTTTGGC 75
QY 69 AATTGGCTTCGAGGCTCAGGCGATGCTCCACTTCGCGCGGATTTGGCTCAGATGAC 128
DB 76 AATTGGAAGAAGATATCCGTTAGTGAAGAATTAGGAGAGATTAATATCATGTGAT 135
QY 129 ATCATGATGCGCATTTTGTCCCAATTAACATTTGGGCTCCAGTTATTGAAGTTG 188
DB 136 GTCATGAGCGTCAATTTGTGCCCCAATTAACCTTAGGACGCAATATGCTTACCGATT 195
QY 189 AAGAAAGCACAAGGACATATTGATTTGTCACCTTAGTTACAAATCTCTGATTAT 248
DB 196 CGTTCAGTGACAAAATCACTATGATGATTTGATTTGATGATTTGCAACTGAAATTAAT 255
QY 249 GTTGAACCTTGGCAAAAGCTGTGCTTCTGTTTACATTTACGTTGAGACATCAAAA 308
DB 256 ATCATATGCTTTTCCGAAAGCGGTGCGATATTATTACCTTCACAAAGCAACACCC 315
QY 309 GATTAACGTAAGAACTTATTCAGAAAGATCAAGTACATGCGATGATTTCTGTGTAGCA 368
DB 316 CATAT---TTCAATCGTCCCTTCAATGATTTAAATGCGGGGTGTAAGCTGGGTAAAC 372
QY 369 TTAAGACCTGGGAGCC 385
DB 373 ATCAATCTGGGACAC 389
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RESULT 11

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US-08-961-527-149
; Sequence 149, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
```

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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 1256 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-149
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Query Match

Best Local Similarity 20.0%; Score 77.6; DB 3; Length 1256;

Matches 189; Conservative 0; Mismatches 164; Indels 3; Gaps 1;

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QY 33 AAAATAGCTCTTGATGATGCTCTTCGAGCTTCGCAATTTGGCTTCGAGCTCAGCC 92
DB 4786 AAGATTGCTCGTAAATTTGCGAGCATATGCAACTTTGAACGTGAATCAACGT 4845
QY 93 ATGCTCACTTCGCGCGCGATTTGCTTCACATGACATCATGATGGGCAATTTGTCGCC 152
DB 4846 CTAGAACCACTGGGGCAGAAATATGCCATATGATATCATGACATGATTTGTACCG 4905
QY 153 AATTACTTTTGGCGCTCCAGTTATTGAAAGTTTGAAGAAAGCACAACAAAGCATATTG 212
DB 4906 CAAATCAGTTTGTGTGAGGTGTGTGAGAGGCTTCGCTCATGTAAAGATGTTTC 4965
QY 213 GATTGTACCTTATGTTTCAAAATCTCTGATTATGTTGAACCTTGGCAAAAGCTGTG 272
DB 4966 GATTGCACCTTATGTTGTCAAAACCTGAGCATCATCTGAAAGATTTTGGCTGAGGT 5025
QY 273 GCTTGTGTTTACATTTACGTTAGACATCAAAAAGATPACTGAAAGACTTATCA 332
DB 5026 GCAAGACATCATGATTCATGATGA---AGCAACCCCTCATATTCATGAGCCCTCCAA 5082
QY 333 AGAATCAAGTCACATGAGCATGATTTCTGTGTAGCATTAAGCTGGGAGCCCCCGT 388
DB 5083 AAAATCGTTCACTGGAGTTAAAGCTTACGTGTTATCAATCTGGGACATCAAGT 5138
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RESULT 12

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US-09-198-452A-1/C
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
```


TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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OTHER INFORMATION: n=a or c or g or t
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LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or t


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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 105..434
FEATURE:
NAME/KEY: misc_feature
LOCATION: 12
OTHER INFORMATION: y=c or t
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NAME/KEY: misc_feature
LOCATION: 13
OTHER INFORMATION: y=c or t
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NAME/KEY: misc_feature
LOCATION: 28
OTHER INFORMATION: y=c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 86
OTHER INFORMATION: k=g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 117
OTHER INFORMATION: k=g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 230
OTHER INFORMATION: w=a or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 291
OTHER INFORMATION: n=a, g, c or t
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 293
OTHER INFORMATION: n=a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 317
OTHER INFORMATION: n=a, g, c or t
FEATURE:
NAME/KEY: UNSURE
LOCATION: 5
OTHER INFORMATION: Xaa=Gly or Trp
FEATURE:
NAME/KEY: UNSURE
LOCATION: 63
OTHER INFORMATION: Xaa=any one of the twenty amino acids
FEATURE:
NAME/KEY: UNSURE
LOCATION: 71
OTHER INFORMATION: Xaa=Asp or Glu
US-09-513-999C-1817

Query Match
Best Local Similarity 55.4%; Score 75.8; DB 4; Length 434;
Matches 201; Conservative 3; Mismatches 149; Indels 10; Gaps 3;

QY 33 AAAATAGCTTCCTTGATGCTCTTCCGACTTCGCAATTTGGCTTCGAG-GCTCAGGC 91
DB 44 AAGATTGGCCCGTCATCTCAACAGCAGCTGGCCCAATTTAKGGCCGAGTGCCCTCCGG 103
QY 92 CATGCTCCACTTCGGCGCGGATTTGCTCAACATGACATCATGATGGCATTTTGTCCC 151
DB 104 GATGCTAGACTCTKGGGCGGATTTATCTGACCTGACGTAATGAGAGGGCATTTTGTCC 163
QY 152 CAATTAACTATTTGGGCTCCAGTTATTTGAAGTTTGAAGAAACA-----CACAAGGC 205
DB 164 CAACATCACTTTTGTGACCTGTGTGTAGAAAGCTTCGAAAGCAGCTAGGCGCAGAGCC 223
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QY 206 ATATTGGATTGTACCTTATGTTAAATCCCTTGATTATGTTGAACCTTGGCAA 265
DB 224 TTTCTTACATGACATGATGTTGTCCAAAGCAGACAGTGGTAAGCCATGCTGT 283
QY 266 AGCTGTCCTTCCTGTTTACATTTACGTAGAGACATCAAAAGATTAACCTGAAAGACT 325
DB 284 AGCAGGMMNNATAGTACACCTTTACCTGCA---NCGTACTGAGAACCCAGGGGCTTT 340
QY 326 TATCCAAAGATCAAGTCAATGATGATGATTTCTGTTAGCATTTAAAGCTTGGACCC 385
DB 341 GATTAAAGACATTCGGGAGAAATGGATGAGGTGGCTTGCCATCAAAACAGAAACCTC 400
QY 386 CGT 388
DB 401 AGT 403

RESULT 15
US-09-902-540-9495
Sequence 9495; Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 9495
LENGTH: 643
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-9495

Query Match
Best Local Similarity 55.3%; Score 75.6; DB 4; Length 643;
Matches 147; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 36 ATAGCTCTTGAGTCTCTTCCGACTTCGCAATTTGGCTTCGAGGCTCAGGCATG 95
DB 4 ATCTCTCTTGCTTTTGTGCTGTGACTTCGGCCGCTTGCCGAGAGGTCCGCGCATC 63
QY 96 CTCACCTCGGCGCGGATTTGGCTCCACATGACATCATGATGGCATTTTGTCCCAT 155
DB 64 GAAGCCGCTGTCGCGGATTTGATTCAGTGCATGATGATGAGGCGGCTTGTGCGAAG 123
QY 156 TTAACATTTGGCGCTCCAGTTATTTGAAGTTGAAGAAAGACACAAGGCATATTTGAT 215
DB 124 ATCAGATTTGGCCCGGTGTGTGTGAGGCGCATCAAGCGGTGCGACAGAGCCCTTGAAC 183
QY 216 TGTCACTTATGTTTAAACATCTCTTGAATTAATGTTGAACCTTGGCAAAAGCTGCTGT 275
DB 184 GTGACACTGATGATTTGTGAGCGGAGCGCTACGTGAGGCTTGTGTAAGGCGGGGGG 243
QY 276 TCTGTTTACATTTACGCTAGAGAC 301
DB 244 GACGTGCTGACGCTGACGCTGAGAGC 269
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	388	100.0	417	11	US-09-987-899-4761
2	370	95.4	837	17	US-10-424-599-109667
3	358.4	92.4	845	17	US-10-424-599-109666
4	261.6	67.4	629	18	US-10-021-323-6163
5	252.2	65.0	266	11	US-09-987-899-4727
6	250.4	64.5	272	11	US-09-987-899-4725
7	247	63.7	499	18	US-10-425-115-92527
8	241.8	62.3	260	11	US-09-987-899-4726
9	239.8	61.8	1406	18	US-10-437-963-45062
10	225.4	58.1	1026	18	US-10-767-701-12139
11	223.8	57.7	1027	17	US-10-425-114-4370

12	223.8	57.7	1250	18	US-10-425-115-155395	Sequence 155395, A
13	219.6	56.6	959	17	US-10-425-114-28690	Sequence 28690, A
14	215.6	55.6	705	17	US-10-393-840-519	Sequence 519, App
15	215	55.4	508	17	US-10-393-840-513	Sequence 513, App
16	213.4	55.0	459	17	US-10-393-840-520	Sequence 520, App
17	211.6	54.5	410	17	US-10-393-840-521	Sequence 521, App
18	208	53.6	502	17	US-10-393-840-514	Sequence 514, App
19	205.8	53.0	228	11	US-09-987-899-4728	Sequence 4728, App
20	202.8	52.3	415	11	US-09-987-899-4723	Sequence 4723, App
21	184.2	47.5	668	18	US-10-425-115-41147	Sequence 41147, A
22	173.8	44.8	363	17	US-10-424-599-11379	Sequence 11379, A
23	165.4	42.6	280	9	US-09-923-876-4114	Sequence 4114, App
24	165.4	42.6	280	10	US-09-923-876-4114	Sequence 4114, App
25	161.8	41.7	269	11	US-09-987-899-4705	Sequence 4705, App
26	159.4	41.1	557	18	US-10-425-115-180354	Sequence 180354, A
27	139.4	35.9	523	17	US-10-424-599-112302	Sequence 112302, A
28	134	34.5	438	17	US-10-424-599-112304	Sequence 112304, A
29	115.6	29.8	791	18	US-10-425-115-155373	Sequence 155373, A
30	108.8	28.0	606	18	US-10-021-323-7334	Sequence 7334, App
31	103.6	26.7	229	11	US-09-987-899-4705	Sequence 4705, App
32	99.4	25.6	193	17	US-10-424-599-43914	Sequence 43914, A
33	91.4	23.6	319630	17	US-10-398-221-7	Sequence 2058, App
34	91.4	23.6	3011208	17	US-10-398-221-2058	Sequence 321, App
35	88.8	22.9	730	17	US-10-037-270-617	Sequence 617, App
36	88.8	22.9	907	15	US-10-117-722-617	Sequence 617, App
37	88.8	22.9	907	17	US-10-117-722-617	Sequence 617, App
38	88.8	22.9	1205	18	US-10-729-473-12	Sequence 12, App1
39	88.8	22.9	4397	18	US-10-357-930-25186	Sequence 25186, A
40	88.8	22.9	4397	18	US-10-357-930-25846	Sequence 25846, A
41	87.2	22.5	876	17	US-10-092-900A-319	Sequence 319, App
42	85	21.9	961	15	US-10-037-270-618	Sequence 618, App
43	85	21.9	961	17	US-10-117-722-618	Sequence 618, App
44	83.6	21.5	916	8	US-08-781-986A-1149	Sequence 1149, App
45	83.6	21.5	916	17	US-10-329-624-1149	Sequence 1149, App

ALIGNMENTS

RESULT 1
US-09-987-899-4761
Sequence 4761, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4761
LENGTH: 417
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3040-057-01-B1-C5
US-09-987-899-4761

Query Match 100.0% Score 388; DB 11; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.7e+110; Indels 0; Gaps 0;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGAGGAAGAAAGAAAGATGGAATGACACCGAAATAGCTCTGATGCTCTTCGCG 60
DB 30 GGAGGAAGAAAGAAAGATGGAATGACACCGAAATAGCTCTGATGCTCTTCGCG 89

```
OY 61 ACTTGCCCAATTTGGCTTCCAGGCTCAGCGCATCTCCACTTGGCGCCGCGATTGGCTCC 120
Db 90 ACTTGCCCAATTTGGCTTCCAGGCTCAGCGCATCTCCACTTGGCGCCGCGATTGGCTCC 149
OY 121 ACATGACATCATGATGGGCAATTTGTCCCAATTTAACTATGGGCGCTCCAGTATTTG 180
Db 150 ACATGACATCATGATGGGCAATTTGTCCCAATTTAACTATGGGCGCTCCAGTATTTG 209
OY 181 AAAGTTGAGAAAGCACAAGGCAATTTGGATTGTCACTTATGGTTACAAATCTC 240
Db 210 AAAGTTGAGAAAGCACAAGGCAATTTGGATTGTCACTTATGGTTACAAATCTC 269
OY 241 TTGATTATGTTGAACCCCTTGGCAAAAGCTGGTGTCTTGCTTTTACATTTTACGTAGAGA 300
Db 270 TTGATTATGTTGAACCCCTTGGCAAAAGCTGGTGTCTTGCTTTTACATTTTACGTAGAGA 329
OY 301 CATCAAAAGATTAAGCTGGAAGAACTTATCCAAAGATCAAGTCAATGATGATGATTCCTG 360
Db 330 CATCAAAAGATTAAGCTGGAAGAACTTATCCAAAGATCAAGTCAATGATGATGATTCCTG 389
OY 361 GTGATGATTAAGCTGGGACCCCGCT 388
Db 390 GTGATGATTAAGCTGGGACCCCGCT 417
```

RESULT 2

```
US-10-424-599-109667
; Sequence 109667, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 109667
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_70042C.1
US-10-424-599-109667
```

Query Match Best Local Similarity 95.4%; Score 370; DB 17; Length 837; Pred. No. 1.6e-104;

Matches 376; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
OY 3 AGAAGAAAGAAAGATGGGATGACACCGAAATATAGCTCCCTGATGCTCTCTCCGAC 62
Db 22 AGAAGAAAGAAAGATGGGATGACACCGAAATATAGCTCCCTGATGCTCTCTCCGAC 81
OY 63 TTCGCCAATTTGGCTTCCGAGGCTCAGCGCATGCTCCACTTGGGCGCGATTGGCTCCAC 122
Db 82 TTCGCCAATTTGGCTTCCGAGGCTCAGCGCATGCTCCACTTGGGCGCGATTGGCTCCAC 141
OY 123 ATGACATCATGATGGGCAATTTGTCCCAATTTAACTATGGGCGCTCCAGTATTTGAA 182
Db 142 ATGACATCATGATGGGCAATTTGTCCCAATTTAACTATGGGCGCTCCAGTATTTGAA 201
OY 183 AGTTGAGAAAGCACAAGGCAATTTGGATTGTCACTTATGGTTACAAATCTCTT 242
Db 202 AGTTGAGAAAGCACAAGGCAATTTGGATTGTCACTTATGGTTACAAATCTCTT 261
OY 243 GATTATGTTGAACCCCTTGGCAAAAGCTGGTGTCTTGCTTTTACATTTTACGTAGAGA 302
Db 262 GATTATGTTGAACCCCTTGGCAAAAGCTGGTGTCTTGCTTTTACATTTTACGTAGAGA 321
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OY 303 TCAAAAGATTAAGCTGGAAGAACTTATCCAAAGATCAAGTCAATGCGCATGATTCCTGAT 362
Db 322 TCAAAAGATTAAGCTGGAAGAACTTATCCAAAGATCAAGTCAATGCGCATGATTCCTGAT 381
OY 363 GTAGCATTTAAAGCTGGGACCCCGCT 388
Db 382 GTAGCATTTAAAGCTGGGACCCCGAT 407
```

RESULT 3

```
US-10-424-599-109666
; Sequence 109666, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 109666
; LENGTH: 845
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_70041C.1
US-10-424-599-109666
```

Query Match Best Local Similarity 92.4%; Score 358.4; DB 17; Length 845; Pred. No. 6.7e-101;

Matches 365; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
OY 3 AGAAGAAAGAAAGATGGGATGACACCGAAATATAGCTCCCTGATGCTCTCTCCGAC 62
Db 59 AGAAGAAAGAAAGATGGGATGACACCGAAATATAGCTCCCTGATGCTCTCTCCGAC 118
OY 63 TTCGCCAATTTGGCTTCCGAGGCTCAGCGCATGCTCCACTTGGGCGCGATTGGCTCCAC 122
Db 119 TTCGCCAATTTGGCTTCCGAGGCTCAGCGCATGCTCCACTTGGGCGCGATTGGCTCCAC 178
OY 123 ATGACATCATGATGGGCAATTTGTCCCAATTTAACTATGGGCGCTCCAGTATTTGAA 182
Db 179 ATGACATCATGATGGGCAATTTGTCCCAATTTAACTATGGGCGCTCCAGTATTTGAA 238
OY 183 AGTTGAGAAAGCACAAGGCAATTTGGATTGTCACTTATGGTTACAAATCTCTT 242
Db 239 AGTTGAGAAAGCACAAGGCAATTTGGATTGTCACTTATGGTTACAAATCTCTT 298
OY 243 GATTATGTTGAACCCCTTGGCAAAAGCTGGTGTCTTGCTTTTACATTTTACGTAGAGA 302
Db 299 GATTATGTTGAACCCCTTGGCAAAAGCTGGTGTCTTGCTTTTACATTTTACGTAGAGA 358
OY 303 TCAAAAGATTAAGCTGGAAGAACTTATCCAAAGATCAAGTCAATGCGCATGATTCCTGAT 362
Db 359 TCAAAAGATTAAGCTGGAAGAACTTATCCAAAGATCAAGTCAATGCGCATGATTCCTGAT 418
OY 363 GTAGCATTTAAAGCTG 378
Db 419 GTAGCATTTAAAGTGTG 434
```

RESULT 4

```
US-10-021-323-6163
; Sequence 6163, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Delkman J111
; APPLICANT: Fench, Paul C.C.
; APPLICANT: Fitcher, Karen L.
```

APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021.323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 6163
LENGTH: 629
TYPE: DNA
ORGANISM: Goseypium hirsutum
FEATURE:
OTHER INFORMATION: Clone ID: LIB3828-016-Q1-K6-B2
US-10-021-323-6163

Query Match 67.4%; Score 261.6; DB 18; Length 629;
Best Local Similarity 81.5%; Pred. No. 8.9e-71;
Matches 303; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 14 AAAGATGGGAATGACACCGAAAAAGCTCTCGATGCTCTCTCCGACTTCCCAATT 73
DB 92 AAAGATGGGTGAACACCAAAAATGCTCCATCCATGCTTTCATCGAATTTTGTAACTT 151
QY 74 GGGTTCGAGGCTGACGGGAGCTCCATCTGCGGCGGCGATTTGGCTCCACATGACATCAT 133
DB 152 AGCATCAAGGCGAAAGCGCATGCTGACCTTGGAAGCTGATGCTTCAATGATGATCAT 211
QY 134 GGATGGGCAATTTTGTCCCAATTTAACTATTTGGCCCTCCAGTTATTTGAAAGTTGAGAAA 193
DB 212 GGATGGGCAATTTTGTCCCAATTTAACTATTTGGCCCTCCAGTTATTTGAAAGTTGAGAAA 271
QY 194 GCACACAAAGGCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 253
DB 272 GCACACAAAGGCAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 331
QY 254 ACCCTTGGCAAAAGCTGTGCTTCTGCTTTTCACTTTACGTAAGACATCAAAAAGATTA 313
DB 332 ACTTTTGGGTAAAGCTGTGCTTCTGCTTTTCACTTTTCACTTTTCACTTTTCACTTTTCACTTTT 391
QY 314 CTGGAAGAAGCTTATCCAAAGATCAAGTCACATGAGCATGATTTCTGGGTAGCATTTAA 373
DB 392 CTGGAAGAAGCTTATCCAAAGATTTAATTTGAAAGGCAATGAGGCTGTGTGCGTTTAA 451
QY 374 GCTTGGGACCCC 385
DB 452 GCTTGGGACACC 463

RESULT 5
US-09-987-899-4727
Sequence 4727, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE OF INVENTION: With the Carbon Assimilation Pathway
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987, 899
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262, 979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076, 712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4727
LENGTH: 266
TYPE: DNA
ORGANISM: Glycine max

FEATURE:
OTHER INFORMATION: Clone ID: 70100767H1
US-09-987-899-4727

Query Match 65.0%; Score 252.2; DB 11; Length 266;
Best Local Similarity 97.0%; Pred. No. 4.8e-68;
Matches 257; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 10 AAGAAAAGATGGGAATGACACCGAAAAAGCTCTCGATGCTCTCTCCGACTTCCGCA 69
DB 2 AAGGAAGATGGGAATGACACCGAAAAAGCTCTCGATGCTCTCTCCGACTTCCGCA 61
QY 70 ATTGGCTTCCGAGGCTGAGGCAATGCTCCATTGCGGCGGATTTGGCTCCACATGACA 129
DB 62 ATTGGCTTCCGAGGCTGAGGCAATGCTCCATTGCGGCGGATTTGGCTCCACATGACA 121
QY 130 TCATGATGGGCAATTTTGTCCCAATTTAACTATTTGGGCTCCAGTTATTTGAAAGTTTGA 189
DB 122 TCATGATGGGCAATTTTGTCCCAATTTAACTATTTGGGCTCCAGTTATTTGAAAGTTTGA 181
QY 190 GAAAGCACAAAGGCAATTTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 249
DB 182 GAAAGCACAAAGGCAATTTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 241
QY 250 TTGAACCTTGGCAAAAGCTGTGC 274
DB 242 TTGAACCTTGGCAAAAGCTGTGC 266

RESULT 6
US-09-987-899-4725
Sequence 4725, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE OF INVENTION: With the Carbon Assimilation Pathway
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987, 899
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262, 979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076, 712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4725
LENGTH: 272
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(272)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 700971857H1
US-09-987-899-4725

Query Match 64.5%; Score 250.4; DB 11; Length 272;
Best Local Similarity 96.9%; Pred. No. 1.8e-67;
Matches 254; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 AAGAAAAGATGGGAATGACACCGAAAAAGCTCTCTCGATGCTCTCTCCGACTTCCGCA 62
DB 11 AAGAAAAGATGGGAATGACACCGAAAAAGCTCTCTCGATGCTCTCTCCGACTTCCGCA 70
QY 63 TTGGCAATTTTGGCTTCCGAGGCTGAGGCAATGCTCCATTGCGGCGGATTTGGCTCCAC 122
DB 71 TTGGCAATTTTGGCTTCCGAGGCTGAGGCAATGCTCCATTGCGGCGGATTTGGCTCCAC 130
QY 123 ATGACATCATGATGGGCAATTTTGTCCCAATTTAACTATTTGGGCTCCAGTTATTTGAA 182

Db 131 ATGCACATCAGATGGGCACTTTGTCCCAATTAACTATGCGCTCCAGTTATTGAA 190
QY 183 AGTTTGAAAGCACACAAAGGCATATTGGATTGTCACTTATGTTAAACATCTCTT 242
Db 191 AGTTTGAAAGCACACAAAGGCATATTGGATTGTCACTTATGTTAAACATCTCTT 250
QY 243 GATTATGTTGAACCTTTGGCAA 264
Db 251 GATTATGTTGAACCTTTGGCAA 272

RESULT 7

US-10-425-115-92527
; Sequence 92527, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 92527
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_184377C.1
US-10-425-115-92527

Query Match 63.7%; Score 247; DB 18; Length 499;
Best Local Similarity 78.7%; Pred. No. 2.8e-66;
Matches 225; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 14 AAGATGGGAATGACACCGAAATAGCTCTTCGATGCTCTTCGCACTTGGCAATT 73
Db 90 AACCATGGCGGGCGGCGGAGATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 149
QY 74 GCTTCCGAGGCTCAGCGGATGCTCACTTGGCGCGGATGCTGCTGCTGCTGCTGCT 133
Db 150 CCGCTCGAGGCGGAGCGGATGCTCGCGCGCGGATGCTGCTGCTGCTGCTGCTGCT 209
QY 134 GGATGGGCACTTTTGTCCCAATTAACTATGCGCTCCAGTTATTGAAAGTTGAGAA 193
Db 210 GGATGGGCACTTCTGCTTCAATTAACTATGCGCTCCAGTTATTGAAAGTTGAGAA 269
QY 194 GCACCAAGGATATTGGATTGTCACTTATGTTAAACATCTCTTGTATTGTTGA 253
Db 270 GCACCAAGGATATTGGATTGTCACTTATGTTAAACATCTCTTGTATTGTTGA 329
QY 254 ACCCTTGGCAAAAGCTGTGCTTCTGTTTCACTTAACTATGCGCTCCAGTTATTGAA 313
Db 330 GCGATTGGAAAAAGCTGTGCTTCTGTTTCACTTAACTATGCGCTCCAGTTATTGAA 389
QY 314 CTGGAAGAACTTATCCAAAGATCACTGATGCGATGCTGCTGCTGCTGCTGCTGCT 373
Db 390 CTGGAAGAACTTATCCAAAGATCACTGATGCGATGCTGCTGCTGCTGCTGCTGCT 449
QY 374 GCGTGGGAGCCCGCT 388
Db 450 GCGTGGTACTCTGT 464

RESULT 8

US-09-987-899-4726
; Sequence 4726, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jindong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 4726
; LENGTH: 260
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701064495H1
US-09-987-899-4726

Query Match 62.3%; Score 241.8; DB 11; Length 260;
Best Local Similarity 97.2%; Pred. No. 8.3e-65;
Matches 246; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 AGAAGAAAGAAAGATGGAATGACACCGAAATAGCTCTTCGATGCTCTTCGAC 62
Db 8 AGACGAAAGAAAGATGGAATGACACCGAAATAGCTCTTCGATGCTCTTCGAC 67
QY 63 TTCCGCAATTTGGCTTCCGAGGCTCAGGCGATGCTCCACTTGGCGCGGATTTGGCTCCAC 122
Db 68 TTCCGCAATTTGGCTTCCGAGGCTCAGGCGATGCTCCACTTGGCGCGGATTTGGCTCCAC 127
QY 123 ATGACATCATGATGAGGCACTTTGTCCCAATTAACTATGCGCTCCAGTTATTGAA 182
Db 128 ATGACATCATGATGAGGCACTTTGTCCCAATTAACTATGCGCTCCAGTTATTGAA 187
QY 183 AGTTTGAAAGCACACAAAGGCATATTGGATTGTCACTTATGTTAAACATCTCTT 242
Db 188 AGTTTGAAAGCACACAAAGGCATATTGGATTGTCACTTATGTTAAACATCTCTT 247
QY 243 GATTATGTTGAC 255
Db 248 GATTATGTTGAC 260

RESULT 9

US-10-437-963-45062
; Sequence 45062, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barabazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 45062
; LENGTH: 1406
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1406)
; OTHER INFORMATION: unsure at all n locations


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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48063C.1
US-10-437-963-45062

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Query Match	61.8%;	Score 239.8;	DB 18;	length 1406;
Best Local Similarity	78.8%;	Pred. No. 8.7e-64;		
Matches 286;	Conservative 0;	Mismatches 77;	Indels 0;	Gaps 0;

Qy	26	GAAACCGAAAAATAGCTCCCTTCGATGCTCTTCCGACTTCGCAATTTGGCTTCGAGGC	85
Db	70	GGGGGGAAGATAGCGCCCGTCCATGCTCTCGTCGACTTCCGCACTCCGCCGGAGGC	129
Qy	86	TCAGCGCATGCTCCACTTCGGCGCGCGAATTGGCTCCACATGACATCATGATGGGCATT	145
Db	130	CGACCGCATGATCGCGCTCGCGCGCGCACTGGCTCCACATGACATCATGAGCGGGCACT	189
Qy	146	TGTCGCCAATTTAACTATTGGCGCGCTCCAGTTATGAAAGTTTGAGAAAGCACACAAAGGC	205
Db	190	TGTTCCCTAATCTACTATTGAGAGCTCCAGTAGTTTCAGAGCTTGAGGAAGCACACAAAGGC	249
Qy	206	ATATTTGGATTGCACTTANAGTTAAACAATCTCTGATATGTTGAACCCCTTGGGAAA	265
Db	250	ATATTTGGACTGCATCTTATGTAACCAATCTTCGATTTATGATAGAACCATTAGCAAA	309
Qy	266	AGCTGAGCTTCTGTTTATCATTTCACTAGAGACATCAAAAGTAACTGGAAGAACT	325
Db	310	AGCTGATGCTCAGGTTTACATTCCATATTAAGATATCCAGAGACATTTGGCAAGAACT	369
Qy	326	TATCCAAAGATCAAGTCACTAGCGATGATTTCTGTGTAGCATTTAAAGCTTGGAGCCC	385
Db	370	CATCCAAAGATCAAGCAAAAGGGTATGGAACCGGTGTATCATTTGAGGCCACGACACTCC	429
Qy	386	CGT 388	
Db	430	TGT 432	

RESULT 10
US-10-767-701-12139
; Sequence 12139, Application US/10767701
; Publication No. US20040172684A1

```

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 12139
LENGTH: 1026
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS13660_1
US-10-767-701-12139

```

Query Match	58.1%;	Score 225.4;	DB 18;	Length 1026;
Best Local Similarity	76.3%;	Pred. No. 2.3e-59;		
Matches 277; Conservative	0;	Mismatches 86;	Indels 0;	

Qy	26	GCACCCGAAATTAAGCTCTTCGATCTCTCTCCACATCGCCAAATTTGGCTTCCGAGGC	85
Db	141	GGGGGGAAAGATAGGCGCGCTGCATCTCTCGTGGACCTTCCCAACTCGCTCTGGAGGC	200
Qy	86	TCAGCGCATGCTTCACCTTGGCGCGCGGANTTGGCTCAATGACATCATGATGAGCAATTT	145
Db	201	TGAGCCCATAGTGTCCGCTCTAGCGCGCCAGCTGGTTACATATGACATCATGATGAGGCACCTT	260
Qy	146	TGCCCCCAATTTAACTATTGGCGCTCCAGTATTGAAGTTTGGAAAGCACAACAAAGGC	205

RESULT 11
US-10-425-114-4370
; Sequence 4370, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128

OTHER INFORMATION: Clone ID: 700355680_FLI
US-10-425-114-4370

Query Match	57.7%	Score 223.8	DB 17	length 1027
Best Local Similarity	76.0%	Pred. No. 7.2e-59		
Matches 276	Conservative	0	Mismatches 87	Indels 0
				Gaps 0

QY	26	GAACCGAAAAATAGCTCCCTTGATGCTCTCTTCCGACCTTGCCCAATTTGGCTTCCGAGGC	85
Dp	172	GGGGGGGAAAGATAGGGCGCGTGSATGCTCTCGTGGGACTTTGGCAACCTGGCTTGGAGGC	231
QY	86	TCAGCGCATGCTCCACTTCCGGGCGGATTTGGCTCCCAATGACATCATGATGGCACTTT	145
Dp	232	TCAGCGCATAGTCCCGCTAGGCGCGACATGGCTCATATATGAGACATCATGATGGGCACTT	291
QY	146	TGTCCCAATTTAACTATTTGGCGCTCCAGTTATTTGAAAGTTTGAAGAAAGCACAAAGGC	205
Dp	292	CGTCTCAACCTCGAATATTTGGGGCGCCGGTGATCACAAGCTTGGAGGAAACATACCAAAGC	351
QY	206	ATATTTGGATTTGCACCTTATGTTTACAATACCTCTTGATTTATGTTAAACCTCTGGCAA	265
Dp	352	ATATTTGGACTGCCATCTTATGTGTACAAAGCCTTCAGATTACGTGAAACCAATTTGGAAA	411
QY	266	AGCTGGTCTTCTGTTTTCATTTCACTGTAAGACATCAAAAGATTACTGGAAGAAACT	325
Dp	412	GGCTGGCGCTTGTGATTCACATTTCCATATATGAAAGTTGCTTAGAGACAACTGGCAAGATCT	471
QY	326	TATCCAAAGATCAAGTCAATGGCATGATTCCTGTGTAGACATTTAAAGCTTGGACCCC	385
Dp	472	CATCCAAAGCATTAATCAAAAGGATATGGCGCTGTGTATCATTTGAGGCGCAAGTACTCC	531
QY	386	CGT	388

Db 532 AGT 534

RESULT 12

US-10-425-115-155395
; Sequence 155395, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 155395
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_7329C.1
US-10-425-115-155395

Query Match 57.7%; Score 223.8; DB 18; Length 1250;
Best Local Similarity 76.0%; Pred. No. 86-59;
Matches 276; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 26 GACACCGAATAATGCTCTCTTCGATGCTCTCTTCGACCTTCGCCAATTGGCTTCGAGGC 85
DB 189 GGGGGGGAAGATGAGCCCGCGATGCTCTCTCTCGCATCTTGCGAACCTGGCTTCGAGGC 248
QY 86 TCAGCGCATGCTCCATCTGGGCGCGCATTTGGCTCCCATGAGCATATGATGGGCATT 145
DB 249 TGAGCGCATGCTCCGCTTCGAGCGCGCATGCTTCATGAGCATATGATGGGCATT 308
QY 146 TGTCCCAATTTAACTATTGGCGCTCCAGTTATTGAAGTTTGAAGACACACAAAGGC 205
DB 309 CGTTCCTAACCTGACTATTTGGGGCTCGGTGATCCAGACTTGAGAAACATACCAAGC 368
QY 206 AATATTGGATGTCACCTTATGTTACAAATCTCTTGAATATGTTAAACCTTGGCAA 265
DB 369 AATATTGGCTCCATCTTATGTTACAAAGCTTCGATTTGAGAACCATTTGAAA 428
QY 266 AGCTGGTCTCTGTTTACATTTCACTAGAGCATCAAAAGATTAATCTGAAAGACT 325
DB 429 GGCTGGCGCTTCTGATTTCAATTCATATAGAGTTGCTAGAGCAACTGGCAAGACT 488
QY 326 TATCCAAAGATCAAGTCACTAGGCACTGATTCCTGGTGTAGCATTTAAAGCTGGAGCCC 385
DB 489 CATCCAAAGCATTAATCAAAAGGTATGCGGCTGTGATCATTTGAGGCCAGGTAATCC 548
QY 386 CGT 388
DB 549 AGT 551

RESULT 13

US-10-425-114-28690
; Sequence 28690, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 28690
; LENGTH: 959
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4762-037-D5_FLI
US-10-425-114-28690

Query Match 56.6%; Score 219.6; DB 17; Length 959;
Best Local Similarity 76.3%; Pred. No. 146-57;
Matches 270; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 26 GACACCGAATAATGCTCTCTTCGATGCTCTCTTCGACCTTCGCCAATTGGCTTCGAGGC 85
DB 126 GGGGGGGAAGATGAGCCCGCTCGATCTCTCTCTCGCATCTTGCGAACCTGGCTTCGAGGC 185
QY 86 TCAGCGCATGCTCCATCTGGGCGCGATTTGGCTCCCATGAGCATATGAGATGGGCATT 145
DB 186 TGAGCGCATGCTCCGCTTCAGGCGCGCATGGCTGATGATGAGCATATGAGATGGGCATT 245
QY 146 TGTCCCAATTTAACTATTGGCGCTCCAGTTATTGAAGTTTGAAGACACACAAAGGC 205
DB 246 CGTTCCTAACCTGACTATTTGGGGCTCGGTGATCCAGACTTGAGAAACATACCAAGC 305
QY 206 AATATTGGATGTCACCTTATGTTACAAATCTCTTGAATATGTTAAACCTTGGCAA 265
DB 306 AATATTGGACGCTCATCTTATGTTACAAAGCTTCGATTTGAGAACCATTTGAAA 365
QY 266 AGCTGGTCTCTGTTTACATTTCACTAGAGCATCAAAAGATTAATCTGAAAGACT 325
DB 366 GGCTGGCGCTTCTGATTTCACTTCAATTAATGAGTTGCTAGAGCAACTGGCAAGACT 425
QY 326 TATCCAAAGATCAAGTCACTAGGCACTGATTCCTGGTGTAGCATTTAAAGCTGG 379
DB 426 CATCCAAAGCATTAATCAAAAGGTATGCGGCTGTGATCATTTGAGGCCAGG 479

RESULT 14

US-10-393-840-519
; Sequence 519, Application US/10393840
; Publication No. US20030229922A1
; GENERAL INFORMATION:
; APPLICANT: Blockberg, Leonard N.
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1012c3
; CURRENT APPLICATION NUMBER: US/10/393,840
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 09/636,800
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/170,862
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 60/148,426
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT NZ/99/00169
; NUMBER OF SEQ ID NOS: 956
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 519
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-393-840-519

Query Match 55.6%; Score 215.6; DB 17; Length 705;
Best Local Similarity 73.5%; Pred. No. 2,1e-56;
Matches 275; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 9 AAGAGAAAGATGGGAATGACACGAAATAAGCTCTTCGATGCTCTTCGACATTCGCC 68

Db 132 AACACAGAGAGGGGTTATCCCTTAATTTGCTCCGTCATGTGTGCATCAGACTTTGGC 191
QY 69 AATTGGCTTCGAGGCTCAGGCATGCTCCACTTGGGCGGATTTGGCTCCACATGAC 128
Db 192 AATCTGGCTTCAGAGGCGAAATATATAGCGAAATGTGCGAGATTGGTGCATATGAC 251
QY 129 ATCATGATGGGCTTTTGTCCCAATTTAATATTGGGCTCCAGTTATGAAAGTTTG 188
Db 252 ATCATGATGGGCTTTTGTCCCAATTTAATATTGGGCTCCAGTTATGAAAGTTTG 311
QY 189 AGAAGACACAAAGGCTATTGTGATGTCACCTATGATTAACAATCCTCTGATTAAT 248
Db 312 AGAAGACATACCAGGCTATTGTGATGTCACCTATGATTAACAATCCTCTGATTAAT 371
QY 249 GTTGAACCTTGGCAAAAGCTGCTGCTTGTGTTTACATTTTACCTAGACATCAAAA 308
Db 372 GTGAGGCCATTGGCAAAAGCTGAGCTTCAGGGTTCATTTTCAATGTGAGGCTGCCAA 431
QY 309 GATTACTGAAAAGAACTTATCCAAAGATCAAGTCATGCGATGATTTCTGTGTAGA 368
Db 432 GACCAATTGGCAAGATCTCATCAAAAGAAATCAGAAATGCTGCGATGCGGCTGAGTGCA 491
QY 369 TTAAGCCTGGGAC 382
Db 492 GTGAACCTGGAAC 505

RESULT 15
US-10-393-840-513
; Sequence 513, Application US/10393840
; Publication No. US2003022922A1
; GENERAL INFORMATION:
; APPLICANT: Blockberg, Leonard N.
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1012c3
; CURRENT APPLICATION NUMBER: US/10/393,840
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 09/636,800
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/170,862
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 60/148,426
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT NZ/99/00169
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 956
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-393-840-513

Query Match 55.4%; Score 215; DB 17; Length 508;
Best Local Similarity 73.3%; Pred. No. 2.7e-56;
Matches 275; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
QY 8 GAAAGAAAAGATGGGAATGACACCGAAATAGCTCCTTGATGCTCTTCCGACTTGGC 67
Db 97 GAACACAGAGAGGGGTTATCCCTTAATTTGCTCCGTCATGTGTGCATCAGACTTTGC 156
QY 68 CAATTGGCTTCGAGGCTCAGGCTCAGGCTCCACTTGGGCGGATTTGGCTCCACATGGA 127
Db 157 GAATCTGGCTTCAGAGGCGAAATATATGACGAAATGATGAGATTTGGTGTATGGA 216
QY 128 CATCATGATGGGCAATTTTGTCCCAATTTAATATTGGGCTCCAGTTATGAAAGTTT 187
Db 217 CATCATGATGGGCAATTTTGTCCCAATTTAATATTGGGCACTGTGATTCAGAGTTT 276
QY 188 GAGAAAGCACAAAGGCAATTTGATTTGACCTTATGTTACAAATCCTCTGATTA 247

Db 277 GAGGAAGCATACCAGGCAATTTGATTTGATCTTAATGTGCACAAACCTCTTGATTA 336
QY 248 TTTGAACCTTGGCAAAAGCTGTGCTTGTGTTTACATTTACGTAAGACATCAAA 307
Db 337 TGTGAGCCATTTGCAAAAGCTGAGCTTCAGGGTTCATTTTCAATGTGAGGCTGCCAA 396
QY 308 AGATACTGAAAAGAACTTATCCAAAGATCAAGTCATGCGATGATTTCTGTGTAGC 367
Db 397 AGACAAATTGGCAAGATCTCATCAAAAGAAATCAGAAATGCTGCGATGCGGCTGAGTGCC 456
QY 368 ATTAAGCCTGGGAC 382
Db 457 AGTGAACCTGGAAC 471

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OM nucleic - nucleic search, using sw model

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Title: US-09-300-482-311

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46.6	17.0	741	4	US-09-583-110-44
2	46.4	16.9	1288	1	US-08-440-856A-9
3	44.6	16.3	77536	4	US-09-410-551B-1
4	44.6	16.3	77536	4	US-09-940-316B-1
5	44.6	16.3	4403765	3	US-09-103-840A-2
6	44.6	16.3	4411529	3	US-09-103-840A-2
7	43	15.7	701	3	US-09-133-321-1
8	43	15.7	753	4	US-09-252-991A-13584
9	43	15.7	765	4	US-09-252-991A-13860
10	43	15.7	4411529	3	US-09-103-840A-1
11	42.8	15.6	2225	4	US-09-902-540-8186
12	42.8	15.6	6301	4	US-09-902-540-8186
13	42.2	15.4	1187	1	US-08-440-856A-2
14	42	15.3	813	4	US-09-252-991A-6615
15	42	15.3	1029	4	US-09-252-991A-6683
16	42	15.3	1974	4	US-09-252-991A-6585
17	42	15.3	2106	4	US-09-252-991A-6717
18	41.8	15.3	833	2	US-08-403-852D-3
19	41.8	15.3	833	3	US-08-510-646B-3
20	41.8	15.3	833	3	US-09-231-818-3
21	41.8	15.3	833	4	US-09-635-359B-3
22	41.8	15.3	882	3	US-08-818-112-138
23	41.8	15.3	882	3	US-08-818-111-138
24	41.8	15.3	882	3	US-09-056-556-138
25	41.8	15.3	882	3	US-09-072-596-133
26	41.8	15.3	882	4	US-09-252-991A-5644
27	41.8	15.3	882	4	US-09-072-967-138

28	41.8	15.3	1020	4	US-09-252-991A-5550	Sequence 5550, Ap
29	41.8	15.3	2079	2	US-09-252-991A-5584	Sequence 5584, Ap
30	41.8	15.3	5392	2	US-08-403-852D-1	Sequence 1, Appl
31	41.8	15.3	5392	3	US-08-510-646B-1	Sequence 1, Appl
32	41.8	15.3	5392	3	US-09-231-818-1	Sequence 1, Appl
33	41.8	15.3	5392	4	US-09-635-359B-1	Sequence 1, Appl
34	41.6	15.2	290	3	US-08-818-112-37	Sequence 37, Appl
35	41.6	15.2	290	3	US-08-818-111-37	Sequence 37, Appl
36	41.6	15.2	290	3	US-09-056-556-37	Sequence 37, Appl
37	41.6	15.2	290	3	US-09-072-596-37	Sequence 37, Appl
38	41.6	15.2	290	4	US-09-072-967-37	Sequence 37, Appl
39	41.6	15.2	1929	3	US-09-380-420C-1	Sequence 1, Appl
40	41.6	15.2	1929	4	US-09-899-642A-1	Sequence 1, Appl
41	41.4	15.1	490	4	US-10-101-464A-286	Sequence 286, App
42	41.4	15.1	1917	4	US-09-902-540-3588	Sequence 3588, Ap
43	41.4	15.1	19394	4	US-09-902-540-1172	Sequence 1172, Ap
44	41.4	15.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl
45	41.2	15.0	987	4	US-09-252-991A-13731	Sequence 13731, A

ALIGNMENTS

```

RESULT 1
US-09-583-110-44
; Sequence 44, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 44
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; US-09-583-110-44

Query Match
Best Local Similarity 66.3%; Pred. No. 0.0077;
Matches 67; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 171 GACGATTTGAGAAATCGCCCTTCAAGAGCGCTGAGTACGTGAGTCCGAGTGTGTC 230
DB 61 GAAATTCGAGAAATGACAGTATCAAGCTGCTGAGTGTGAGCAGTGAATGTGTC 120
QY 231 CTCGCGCTTAGCAGCGCTTCCACCGCAAGCATGCGGTGCA 271
DB 121 GTTGAGCTTGAAGACGAGCTGAGCTGCTATATTTGTGCA 161

RESULT 2
US-08-440-856A-9
; Sequence 9, Application US/08440856A
; Patent No. 5750873
; GENERAL INFORMATION:
; APPLICANT: DELLAPORTA, STEPHEN L.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
; TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVE. N.W.
; CITY: WASHINGTON

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/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/440,856A
/ FILING DATE: 15-MAY-1995
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MILLMAN, ROBERT A.
/ REGISTRATION NUMBER: 36,217
/ REFERENCE/DOCKET NUMBER: 05463-20001.00
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1517
/ TELEFAX: (202) 887-0763
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1288 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-440-856A-9

Query Match      16.3%; Score 46.4; DB 1; Length 1288;
Best Local Similarity 48.3%; Pred. No. 0.01;
Matches 86; Conservative 13; Mismatches 79; Indels 0; Gaps 0;

QY 97 TCATGCCACCGAAGAAAGCCGATGAGAGCGGCTCTCTCCACCCCTCTCTCCCTCCG 156
Db 666 TCTCCGTCGCGACGCTGCGSGGCTCTGCGGCTCGCGCCGCTTACCGCTACCGCTCT 725
QY 157 TCATCTCTACCCCAAGACGATTTGAAGAAATCGCCGCTTACAAGCGCGTCAAGTACG 216
Db 726 CCAAGACGCCATCGTSGGGCTCACCAAGACCGCGCTTCCAGTCTSSGGCGSCACGG 785
QY 217 AGTCGGGATGTCCTCTGCGGCTTACGACCGGCTTCCACCGCCCAAGCATGCGTCA 274
Db 786 TCCGSGTCAACTGCTCTCTGCGGCTTCCGCGTCCGACGCGCCSCTATGCTCATCA 843

RESULT 3
US-09-410-551B-1/c
/ Sequence 1, Application US/09410551B
/ Patent No. 6503737
/ GENERAL INFORMATION:
/ APPLICANT: KOSAN BIOSCIENCES, Inc.
/ APPLICANT: REEVES, CHRISTOPHER
/ APPLICANT: CHU, DANIEL
/ APPLICANT: KHOSLA, CHAITAN
/ APPLICANT: SANTI, DANIEL
/ APPLICANT: WU, KAI
/ TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
/ FILE REFERENCE: 30062-20026.00
/ CURRENT APPLICATION NUMBER: US/09/410,551B
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: US 60/139,650
/ PRIOR FILING DATE: 1999-06-17
/ PRIOR APPLICATION NUMBER: US 60/123,810
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 60/102,748
/ PRIOR FILING DATE: 1998-10-02
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 77536
/ TYPE: DNA
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/ ORGANISM: Streptomyces hygroscopicus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52275)...(71465)
/ US-09-410-551B-1

Query Match      16.3%; Score 44.6; DB 4; Length 77536;
Best Local Similarity 53.1%; Pred. No. 0.085;
Matches 95; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 96 TTGATCGCCACCGAAGAAAGCCGATGAGACGCGGCTCTCTCCACCCCTCTCTCCCTCC 155
Db 46351 TACTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 46292
QY 156 GTCATCTCACCCCAAGACGATTTGAAGAAATCGCCGCTTACAAGCGCGTCAAGTACG 215
Db 46291 GCCGAAGTGGCCACTTCTCTGACGACATCGCGCGGACCGTGTCTGTACACGAAACC 46232
QY 216 GAGTCGGGATGTCCTTGGGCTTACGACCGGCTTCCACCGCCCAAGCATGCGTCA 274
Db 46231 CACTTCGACACGAGTGGCGCGACCGGCAACCGACCGCACCGTGTCTGTCTGGGCGCG 46173

RESULT 4
US-09-940-316B-1/c
/ Sequence 1, Application US/09940316B
/ Patent No. 6759536
/ GENERAL INFORMATION:
/ APPLICANT: KOSAN BIOSCIENCES, Inc.
/ APPLICANT: REEVES, CHRISTOPHER
/ APPLICANT: CHU, DANIEL
/ APPLICANT: KHOSLA, CHAITAN
/ APPLICANT: SANTI, DANIEL
/ APPLICANT: WU, KAI
/ TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE FK-520 POLYKETIDE SYNTH
/ FILE REFERENCE: 30062-20026.11
/ CURRENT APPLICATION NUMBER: US/09/940,316B
/ PRIOR FILING DATE: 2001-08-27
/ PRIOR APPLICATION NUMBER: 09/410,551
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: US 60/139,650
/ PRIOR FILING DATE: 1999-06-17
/ PRIOR APPLICATION NUMBER: US 60/123,810
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 60/102,748
/ PRIOR FILING DATE: 1998-10-02
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 77536
/ TYPE: DNA
/ ORGANISM: Streptomyces hygroscopicus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (52275)...(71465)
/ US-09-940-316B-1

Query Match      16.3%; Score 44.6; DB 4; Length 77536;
Best Local Similarity 53.1%; Pred. No. 0.085;
Matches 95; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 96 TTGATCGCCACCGAAGAAAGCCGATGAGACGCGGCTCTCTCCACCCCTCTCTCCCTCC 155
Db 46351 TACTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 46292
QY 156 GTCATCTCACCCCAAGACGATTTGAAGAAATCGCCGCTTACAAGCGCGTCAAGTACG 215
Db 46291 GCCGAAGTGGCCACTTCTCTGACGACATCGCGCGGACCGTGTCTGTACACGAAACC 46232
QY 216 GAGTCGGGATGTCCTTGGGCTTACGACCGGCTTCCACCGCCCAAGCATGCGTCA 274
Db 46231 CACTTCGACACGAGTGGCGCGACCGGCAACCGACCGCACCGTGTCTGTCTGGGCGCG 46173
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RESULT 5
US-09-103-840A-2
/ Sequence 2, Application US/09103840A
/ Patent No. 6294328
/ GENERAL INFORMATION:
/ APPLICANT: FLEISCHMAN, Robert D.
/ APPLICANT: WHITE, Owen R.
/ APPLICANT: FRASER, Claire M.
/ APPLICANT: VENTER, John C.
/ TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
/ FILE REFERENCE: 24366-20007.00
/ CURRENT APPLICATION NUMBER: US/09/103, 840A
/ CURRENT FILING DATE: 1998-06-24
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 4403765
/ TYPE: DNA
/ ORGANISM: Mycobacterium tuberculosis
/ FEATURE:
/ OTHER INFORMATION: CDC 1551
/ OTHER INFORMATION: "n" bases at various positions throughout the sequence
/ OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match
Best Local Similarity 51.8%, Score 44.6, DB 3, Length 4403765,
Matches 101, Conservative 0, Mismatches 94, Indels 0, Gaps 0,

QY 78 GCCATTCCCTACCCCATTTATGCGCCACGAGAAAGCCGCCATGAGCGCGGCTCTC 137
Db 1632416 GCCGCGCCACCGGTCGCCGCCGCCGCCCAAGTCTCCGCCCGCGCGCGCGCGCC 1632475
QY 138 CACCCCTCTCCCTCCCTCCGTCATCCTACCCAGACGATTTGAAGAAATGCGCGCTAC 197
Db 1632476 CGCCCGCCACCGCCGCTTCTGCGCTGTGCGGATTCGCCCGCGGTGTGGCGA 1632535
QY 198 AAGGCGCTGAGTACGTGAGTCCGGCATGTGCTCGGCTTAGGACACCGGCTCCAGCC 257
Db 1632536 GAAGCGGCGACACCGGCGCATGCGCTCCCGCTTTGGCGCGCGCGCATTAACAC 1632595
QY 258 AAGCATGCCGCTCGAC 272
Db 1632596 AAGCGCGCGCTTGCC 1632610

RESULT 6
US-09-103-840A-1
/ Sequence 1, Application US/09103840A
/ Patent No. 6294328
/ GENERAL INFORMATION:
/ APPLICANT: FLEISCHMAN, Robert D.
/ APPLICANT: WHITE, Owen R.
/ APPLICANT: FRASER, Claire M.
/ APPLICANT: VENTER, John C.
/ TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
/ FILE REFERENCE: 24366-20007.00
/ CURRENT APPLICATION NUMBER: US/09/103, 840A
/ CURRENT FILING DATE: 1998-06-24
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 4411529
/ TYPE: DNA
/ ORGANISM: Mycobacterium tuberculosis
/ OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
16.3%, Score 44.6, DB 3, Length 4411529;

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[illegible]

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US-09-902-540-8186
Sequence 8186, Application US/09902540
Patent No. 6833447


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: GENERAL INFORMATION:
: APPLICANT: Goldman, Barry S.
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Slater, Steven C.
: APPLICANT: Wiegand, Roger C.
: TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
: FILE REFERENCE: 38-10(15849)B
: CURRENT APPLICATION NUMBER: US/09/902,540
: PRIORITY FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: 60/217,883
: PRIOR FILING DATE: 2000-07-10
: NUMBER OF SEQ ID NOS: 16825
:
: SEQ ID NO 8186
: LENGTH: 2225
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: TYPE: DNA
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: ORGANISM: Myxococcus xanthus
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: US-09-902-540-8186

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/ Sequence 6615, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 6615
/ LENGTH: 813
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6615
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Query Match 15.3% Score 42; DB 4; Length 813;
Best Local Similarity 48.0%; Pred. No. 0.12;
Matches 120; Conservative 0; Mismatches 130; Indels 0; Gaps 0;
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QY 18 ACCACACATTCAATTGAACTCTGGAGCTGCTAGCTTCAACTTTAATTACATG 77
DB 545 ACCGCGACAAACTGACGACGAGTCTGCACTGTGTGTAAGCTCGAACTTTGATG 486
QY 78 GCCATTCCCTACCCCATTTTCATCGCCACCGAAGACCGCCATGAGCGGCTCTTC 137
DB 485 GCCAATCCGACGACGAGCTCCAAACCGACCAACAGCGCTCGCCGCGATCAACGAACTC 426
QY 138 CACCCCTCTCCCTCCCTCCGTCATCTCACCCAGACGATTTGAAGAAATCGCCCTAC 197
DB 425 GGGCGCGCGCGCCAGGAAATCGCCGCAACGCCCGCATGCCCTCGACATGCTTCGAC 366
QY 198 AAGCGCTGAGTAGTGAAGTCCGACATGCTCTCGGCTTAGGCAACCGCTTCACCGCC 257
DB 365 GCCAACCAACAGCGCCGAGGACGCAACAGTGTGACAGACCATTCGCGCGATGAAC 306
QY 258 AAGCATGCCG 267
DB 305 GAGCTTTCCG 296
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RESULT 15

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US-09-252-991A-6683
/ Sequence 6683, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 6683
/ LENGTH: 1029
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6683
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Query Match 15.3% Score 42; DB 4; Length 1029;
Best Local Similarity 48.0%; Pred. No. 0.13;
Matches 120; Conservative 0; Mismatches 130; Indels 0; Gaps 0;
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QY 18 ACCACACATTCAATTGAACTCTGGAGCTGCTAGCTTCAACTTTAATTACATG 77
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Search completed: May 4, 2005, 12:28:35
Job time : 97.177 secs

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DB 74 ACCGCGACAAACTGACGACGCTCTGCAACTGTGTGTAAGCCTCGAACTTTGATG 133
QY 78 GCCATTCCCTACCCCATTTTCATCGCCACCGAAGACCGCCATGAGCGGCTCTTC 137
DB 134 GCCAATCCGACGACGAGCTCCAAACCGACCAACAGGCTCGCGCGCATCAACGAACTC 193
QY 138 CACCCCTCTCCCTCCCTCCGTCATCTCAACCAAGACGATTTGAAGAAATCGCCCTAC 197
DB 194 GGGCGCGCGCGCCAGGAAATCGCCGCAACGCGCGCATGCTTCGACATGCTTCGAC 253
QY 198 AAGCGCTGAGTAGTGAAGTCCGACATGCTCTCGGCTTAGGCAACCGCTTCACCGCC 257
DB 254 GCCAACCAACAGCGCCGAGGACGCAACAGTGTGACAGACCATTCGCGCGATGAAC 313
QY 258 AAGCATGCCG 267
DB 314 GAGCTTTCCG 323
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 310.867 Seconds
(without alignments)
5365.716 Million cell updates/sec

Title: US-09-300-482-311

Perfect score: 274
Sequence: 1 cttaatccttcttccacc.....gccaaagcatgcctgcagccg 274

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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22:	/cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	274	100.0	274	11	US-09-987-899-4776
2	264.4	96.5	1422	17	US-10-425-114-15993
3	249	90.9	263	11	US-09-987-899-4775
4	230	83.9	1839	17	US-10-424-599-32036
5	189.6	69.2	1281	18	US-10-739-930-3349
6	189.6	69.2	1495	17	US-10-424-599-32035
7	160.2	58.5	244	17	US-10-424-599-32035
8	98	35.8	291	11	US-09-987-899-4779
9	93.8	34.2	265	11	US-09-987-899-4780
10	86.2	31.5	1027	18	US-10-739-930-3800
11	86	31.4	260	11	US-09-987-899-4781

12	86	31.4	705	18	US-10-425-115-133620	Sequence 133620,
13	86	31.4	1146	17	US-10-424-599-132085	Sequence 132085,
14	81.4	29.7	798	9	US-09-938-842A-656	Sequence 656, App
15	81.4	29.7	798	11	US-09-938-842A-656	Sequence 656, App
16	74.4	27.2	251	17	US-10-424-599-135774	Sequence 135774,
17	69.4	25.3	1116	18	US-10-767-701-12123	Sequence 12123, A
18	64.8	23.6	1304	18	US-10-437-963-85192	Sequence 85192, A
19	63.6	23.2	436	17	US-10-424-599-36084	Sequence 36084, A
20	62.6	22.8	1585	18	US-10-425-115-138187	Sequence 138187,
21	62.6	22.8	1606	18	US-10-739-930-2972	Sequence 2972, App
22	62.4	22.8	333	11	US-09-987-899-4766	Sequence 4766, App
23	62.4	22.8	333	18	US-10-425-115-139573	Sequence 39573, A
24	61	22.3	1068	18	US-10-425-115-138189	Sequence 138189,
25	59.4	21.7	267	11	US-09-987-899-4765	Sequence 4765, App
26	59.4	21.7	1004	18	US-10-739-930-2974	Sequence 2974, App
27	59.4	21.7	1480	18	US-10-739-930-2973	Sequence 2973, App
28	55.2	20.1	227	18	US-10-767-701-152	Sequence 152, App
29	54.6	19.9	4025	18	US-10-437-963-97674	Sequence 97674, A
30	50.4	18.4	299	17	US-10-424-599-84599	Sequence 84599, A
31	50.2	18.3	1060	17	US-10-425-114-6710	Sequence 6710, App
32	50.2	18.3	1136	17	US-10-425-114-35167	Sequence 35167, A
33	50.2	18.3	1392	18	US-10-425-115-107438	Sequence 107438,
34	49.6	18.1	454	9	US-09-734-569-113	Sequence 113, App
35	48.2	17.6	951	15	US-10-156-761-719	Sequence 719, App
36	48.2	17.6	9025608	15	US-10-156-761-1	Sequence 1, Appl
37	48	17.5	796	18	US-10-437-963-40252	Sequence 40252, A
38	46.6	17.0	1128	18	US-10-437-963-96984	Sequence 96984, A
39	46.4	16.9	1206	18	US-10-437-963-85516	Sequence 85516, A
40	46.2	16.9	985	18	US-10-363-345A-31407	Sequence 31407, A
41	46.2	16.9	985	18	US-10-363-345A-31407	Sequence 31407, A
42	46.2	16.9	985	19	US-10-363-483A-31407	Sequence 31407, A
43	46.2	16.9	985	19	US-10-363-483A-31408	Sequence 31408, A
44	45.8	16.7	1055	18	US-10-739-930-4926	Sequence 4926, App
45	45	16.4	2731748	18	US-10-297-465A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-987-899-4776
Sequence 4776, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jingdong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4776
LENGTH: 274
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700745725H1
US-09-987-899-4776

Query Match 100.0%, Score 274, DB 11, Length 274;

Best Local Similarity 100.0%, Pred. No. 6e-75, Mismatches 0, Indels 0, Gaps 0;

Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTTACATTCCTTCTTCCACACACATTCATTTGAACTTGAGAGGCTAGCTTCA	60
DB	1	CTTACATTCCTTCTTCCACACACATTCATTTGAACTTGAGAGGCTAGCTTCA	60


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QY 77 GGGCATTCCTTACCCCATTTTCAATTCGCGACCGAAGACCCGCATGTAGCGCGCTCTCT 136
Db 63 GGGCATTCCTTACCCCATTTTCAATTCGCGACCGAAGACCGAAGGTGCGCATGTAGCGAGGTCTCT 122
QY 137 CAACCCCTCTCCCTCCCTCGCTCATCTTCAACCCAGACGATTTGAAAGAAAT-GCGCGCT 195
Db 123 GCACCCCTCTCTCCCTCTCGCTTATCTCAACCGACGACATTTATGAAATCCAGCGCC 182
QY 196 ACAAGGCGCTCGAGTACGTAGATTCGCGCATGTCTCGGCTTAGGACCGGCTCCACCG 255
Db 183 ACAAGGCGCGGTACGTACCAAAAGTCCGCTGTGCGCTTGGCATGAGCACCGGCTTACCG 242
QY 256 CC 257
Db 243 CC 244

RESULT 8
US-09-987-899-4779
/ Sequence 4779, Application US/09987899
/ Publication No. US20040116682A1
/ GENERAL INFORMATION:
/ APPLICANT: Cheikh, Noridine
/ APPLICANT: Liu, Jingtong
/ APPLICANT: Miller, Phillip W.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
/ FILE REFERENCE: 16517.258
/ CURRENT APPLICATION NUMBER: US/09/987,899
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: US 09/262,979
/ PRIOR FILING DATE: 1999-03-04
/ PRIOR APPLICATION NUMBER: US 60/076,712
/ NUMBER OF SEQ ID NOS: 7341
/ SEQ ID NO 4779
/ LENGTH: 291
/ TYPE: DNA
/ ORGANISM: glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(291)
/ OTHER INFORMATION: unsure at all n locations
/ OTHER INFORMATION: Clone ID: 700562390H1
US-09-987-899-4779

Query Match 35.8%; Score 98; DB 11; Length 291;
Best Local Similarity 97.0%; Pred. No. 2.7e-20;
Matches 98; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 174 GATTGAAAGAAATATCGCCGCTTACAGGCGCTGCGAGTACGTGAGTCCGGCATGCTCTC 233
Db 1 GATTGAAAGAAATATCGCNGCCTTACAGGCGCTGCGAGTACGTGAGTCCGGCATGCTCTC 60
QY 234 GGCCTAGGACACGGGCTCCACCGCCAGAGATCCGCTGACCG 274
Db 61 GGCCTAGGACACGGGCTCCANCGCCAGCATCGCTGANGC 101

RESULT 9
US-09-987-899-4780
/ Sequence 4780, Application US/09987899
/ Publication No. US20040116682A1
/ GENERAL INFORMATION:
/ APPLICANT: Cheikh, Noridine
/ APPLICANT: Liu, Jingtong
/ APPLICANT: Miller, Phillip W.
/ APPLICANT: O Connell, Keith M.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
/ FILE REFERENCE: 16517.258
/ CURRENT APPLICATION NUMBER: US/09/987,899

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/ CURRENT FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: US 09/262,979
/ PRIOR FILING DATE: 1999-03-04
/ PRIOR APPLICATION NUMBER: US 60/076,712
/ PRIOR FILING DATE: 1998-03-06
/ NUMBER OF SEQ ID NOS: 7341
/ SEQ ID NO 4780
/ LENGTH: 265
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700961206H1
US-09-987-899-4780

Query Match
Best Local Similarity 93.3%; Pred. No. 5, 4e-19;
Matches 98; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 10
US-10-739-930-3800
/ Sequence 3800, Application US/10739930
/ Publication No. US20040216190A1
/ GENERAL INFORMATION:
/ APPLICANT: Kovalic, David K.
/ TITLE OF INVENTION: NOCLETIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
/ FILE REFERENCE: 38-21(53377)B
/ CURRENT APPLICATION NUMBER: US/10/739,930
/ CURRENT FILING DATE: 2003-12-18
/ NUMBER OF SEQ ID NOS: 11088
/ SEQ ID NO 3800
/ LENGTH: 1027
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER7422_2
US-10-739-930-3800

Query Match
Best Local Similarity 31.5%; Score 86.2; DB 18; Length 1027;
Matches 106; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

RESULT 11
US-09-987-899-4781
/ Sequence 4781, Application US/09987899
/ Publication No. US20040116682A1
/ GENERAL INFORMATION:
/ APPLICANT: Cheikh, Nordine
/ APPLICANT: Liu, Jingtong
/ APPLICANT: Miller, Phillip W.
/ APPLICANT: O'Connell, Keith M.

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;/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
;/ FILE OF INVENTION: With the Carbon Assimilation Pathway
;/ FILE REFERENCE: 16517,258
;/ CURRENT APPLICATION NUMBER: US/09/987,899
;/ CURRENT FILING DATE: 2001-11-16
;/ PRIOR APPLICATION NUMBER: US 09/262,979
;/ PRIOR FILING DATE: 1999-03-04
;/ PRIOR APPLICATION NUMBER: US 60/076,712
;/ PRIOR FILING DATE: 1998-03-06
;/ NUMBER OF SEQ ID NOS: 7341
;/ SEQ ID NO 4781
;/ LENGTH: 260
;/ TYPE: DNA
;/ ORGANISM: Glycine max
;/ FEATURE:
;/ OTHER INFORMATION: Clone ID: 701120413H1
US-09-987-899-4781

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Best Local Similarity 75.4%; Pred. No. 1.4e-16;
Matches 107; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 131 CCTCTCCACCCCTCTCCCTCCCTCATCTCACCACCAAGAGATTGAAGAAATCGC 190
DB 68 CCACTCCCTCCCTCCCTCCCTCCCTCATCTCACCACCAAGAGATTGAAGAAATCGC 127

QY 191 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTAGGACCGGCTC 250
DB 128 CCGCCGACAAGGCGGTGAGTAGTCCGTCAACAGCGCATGTCTCTCGGCTTAGGACCGGCTC 187

QY 251 CACCGCAAGCATGCCGTGAC 272
DB 188 CACTGCTGCTTCTGTGTGCGC 209

RESULT 12
US-10-425-115-133620
;/ Sequence 133620, Application US/10425115
;/ Publication No. US20040214272A1
;/ GENERAL INFORMATION:
;/ APPLICANT: La Rosa, Thomas J.
;/ APPLICANT: Kovalic, David K.
;/ APPLICANT: Zhou, Yihua
;/ APPLICANT: Cao, Yongwei
;/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;/ FILE OF INVENTION: Plants
;/ FILE REFERENCE: 38-21(53222)B
;/ CURRENT APPLICATION NUMBER: US/10/425,115
;/ CURRENT FILING DATE: 2003-04-28
;/ NUMBER OF SEQ ID NOS: 369326
;/ SEQ ID NO 133620
;/ LENGTH: 705
;/ TYPE: DNA
;/ ORGANISM: Zea mays
;/ FEATURE:
;/ NAME/KEY: unsure
;/ LOCATION: (1)..(705)
;/ OTHER INFORMATION: unsure at all n locations
;/ OTHER INFORMATION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
US-10-425-115-133620

Query Match 31.4%; Score 86; DB 18; Length 705;
Best Local Similarity 75.4%; Pred. No. 1.8e-16;
Matches 107; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 131 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTAGGACCGGCTC 190
DB 176 CCACTCCCTCCCTCCCTCCCTCCCTCATCTCACCACCAAGAGATTGAAGAAATCGC 235

QY 191 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTAGGACCGGCTC 250
DB 236 CCGCCGACAAGGCGGTGAGTAGTCCGTCAACAGCGCATGTCTCTCGGCTTAGGACCGGCTC 295

QY 251 CACCGCAAGCATGCCGTGAC 272
DB 296 CACTGCTGCTTCTGTGTGCGC 317

RESULT 13
US-10-424-599-132085
;/ Sequence 132085, Application US/10424599
;/ Publication No. US20040031072A1
;/ GENERAL INFORMATION:
;/ APPLICANT: La Rosa, Thomas J.
;/ APPLICANT: Kovalic, David K.
;/ APPLICANT: Zhou, Yihua
;/ APPLICANT: Cao, Yongwei
;/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;/ FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;/ FILE REFERENCE: 38-21(53223)B
;/ CURRENT APPLICATION NUMBER: US/10/424,599
;/ CURRENT FILING DATE: 2003-04-28
;/ NUMBER OF SEQ ID NOS: 285684
;/ SEQ ID NO 132085
;/ LENGTH: 1146
;/ TYPE: DNA
;/ ORGANISM: Glycine max
;/ FEATURE:
;/ NAME/KEY: unsure
;/ LOCATION: (1)..(1146)
;/ OTHER INFORMATION: unsure at all n locations
;/ OTHER INFORMATION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
US-10-424-599-132085

Query Match 31.4%; Score 86; DB 17; Length 1146;
Best Local Similarity 75.4%; Pred. No. 2.1e-16;
Matches 107; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 131 CCTCTCCACCCCTCTCCCTCCCTCATCTCACCACCAAGAGATTGAAGAAATCGC 190
DB 247 CCACTCCCTCCCTCCCTCCCTCCCTCATCTCACCACCAAGAGATTGAAGAAATCGC 306

QY 191 CCGCTTACAAGGCGGTGAGTAGTGGAGTCCGGCATGTCTCTCGGCTTAGGACCGGCTC 250
DB 307 CCGCCGACAAGGCGGTGAGTAGTCCGTCAACAGCGCATGTCTCTCGGCTTAGGACCGGCTC 366

QY 251 CACCGCAAGCATGCCGTGAC 272
DB 367 CACTGCTGCTTCTGTGTGCGC 388

RESULT 14
US-09-938-842A-656
;/ Sequence 656, Application US/09938842A
;/ Patent No. US20020160378A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Harper, Jeff
;/ APPLICANT: Krieps, Joel
;/ APPLICANT: Wang, Xun
;/ APPLICANT: Zhu, Tong
;/ TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;/ FILE OF INVENTION: SAME, AND METHODS OF USE
;/ FILE REFERENCE: SRIPI300-3
;/ CURRENT APPLICATION NUMBER: US/09/938,842A
;/ CURRENT FILING DATE: 2001-08-24
;/ PRIOR APPLICATION NUMBER: US 60/227,866
;/ PRIOR FILING DATE: 2000-08-24
;/ PRIOR APPLICATION NUMBER: US 60/264,647
;/ PRIOR FILING DATE: 2001-01-16
;/ PRIOR APPLICATION NUMBER: US 60/300,111
;/ PRIOR FILING DATE: 2001-06-22
;/ NUMBER OF SEQ ID NOS: 5379
;/ SEQ ID NO 656
;/ LENGTH: 798

TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-656

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Job time : 316.867 secs

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Best Local Similarity 64.7%; Pred. No. 5,1e-15;
Matches 121; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 88 ACCCCCATTTTCATGCGCCAGGAAAGCCGCATGAGCCGCCCTCTCCACCCCTCCT 147
DB 17 ATCTCTCTTCAATGACATCGGACAAATCTTGTCCGCTTGAATGTGCTTCAACCGC 76
QY 148 CCCCCCTCCATCCTCACCAGACGATTTGAAGAAATGCGCCCTACAGGCGTCG 207
DB 77 CTCAGGCCCATGAATTAAACAGACGAGCTCAAGCTATGCGCGCTTACAAAGCGTGG 136
QY 208 AGTAGTGAGTCCGCGATGCTCTCGGCTTAGGCAACGCGCTCACCGCCAGCATGCGG 267
DB 137 AATTGCGAGTCCGCGATGTTCTCGGCTCGGAAACGCGCTCACCGCCAAACAGCGCG 196
QY 268 TCGACCG 274
DB 197 TCGACCG 203

RESULT 15
US-09-938-842A-656
Sequence 656, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 656
LENGTH: 798
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-656

Query Match 29.7% Score 81.4; DB 11; Length 798;
Best Local Similarity 64.7%; Pred. No. 5,1e-15;
Matches 121; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 88 ACCCCCATTTTCATGCGCCAGGAAAGCCGCATGAGCCGCCCTCTCCACCCCTCCT 147
DB 17 ATCTCTCTTCAATGACATCGGACAAATCTTGTCCGCTTGAATGTGCTTCAACCGC 76
QY 148 CCCCCCTCCATCCTCACCAGACGATTTGAAGAAATGCGCCCTACAGGCGTCG 207
DB 77 CTCAGGCCCATGAATTAAACAGACGAGCTCAAGCTATGCGCGCTTACAAAGCGTGG 136
QY 208 AGTAGTGAGTCCGCGATGCTCTCGGCTTAGGCAACGCGCTCACCGCCAGCATGCGG 267
DB 137 AATTGCGAGTCCGCGATGTTCTCGGCTCGGAAACGCGCTCACCGCCAAACAGCGCG 196
QY 268 TCGACCG 274
DB 197 TCGACCG 203

GenCore version 5.1.6
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Run on: May 4, 2005, 12:02:12 ; Search time 112.658 Seconds
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170.4	44.3	2629	2	US-09-012-030-1
2	170.4	44.3	2629	2	US-08-590-454-1
3	116.2	30.2	2007	4	US-09-252-991A-3308
4	116.2	30.2	2229	4	US-09-252-991A-3240
5	116.2	30.2	2709	4	US-09-252-991A-3326
6	114.6	29.8	1998	3	US-09-382-106-1
7	106.2	27.6	2085	4	US-09-489-039A-1895
8	100.4	26.1	2127	4	US-09-489-039A-4813
9	99	25.7	35881	4	US-08-311-731A-127
10	93.8	25.4	6895	4	US-09-531-266-1
11	85.8	22.3	4403765	3	US-09-103-840A-2
12	85.8	22.3	4411529	3	US-09-103-840A-1
13	82.8	21.43	2143	3	US-09-064-693A-18
14	82.8	21.5	6641	3	US-09-064-693A-25
15	80.6	20.9	11443	3	US-08-961-527-49
16	80	20.8	1953	4	US-08-956-171E-374
17	80	20.8	1953	4	US-08-781-986A-374
18	78.2	20.3	1968	3	US-09-298-724-1
19	78.2	20.3	1971	4	US-09-583-110-597
20	78.2	20.3	1980	4	US-09-107-433-1392
21	76.8	19.9	1995	5	PCT-US96-0530A-1025
22	76.8	19.9	1830121	4	US-09-557-884-1
23	76.8	19.9	1830121	4	US-09-643-990A-1
24	76.4	19.0	1950	3	US-09-134-001C-2382
25	73	17.7	1230230	4	US-09-107-532A-644
26	68	17.7	1230230	4	US-09-438-185A-1
27	65.8	17.1	1854	4	US-09-107-433-1393

28	65.8	17.1	1977	4	US-09-583-110-2082	Sequence 2082, Ap
29	64.2	16.7	837	4	US-09-134-000C-201	Sequence 201, Ap
30	63.6	16.5	1998	4	US-09-543-681A-1706	Sequence 1706, Ap
31	63	16.4	1738	3	US-08-858-207A-35	Sequence 35, Ap
32	56.8	14.8	1230025	4	US-09-198-452A-1	Sequence 1, Appli
33	53.8	14.0	946	3	US-08-961-527-239	Sequence 239, App
34	51.8	13.5	1329	4	US-09-252-991A-3367	Sequence 3367, Ap
35	51.6	13.4	1359	4	US-09-252-991A-3294	Sequence 3294, Ap
36	51.6	13.4	1377	4	US-09-252-991A-3340	Sequence 3340, Ap
37	51.6	13.4	1710	4	US-09-252-991A-3383	Sequence 3383, Ap
38	51.6	13.4	1872	2	US-08-743-637B-17	Sequence 17, Appl
39	51.6	13.4	1872	3	US-08-526-840B-17	Sequence 17, Appl
40	48.2	12.5	615	4	US-09-540-236-214	Sequence 214, App
41	48.2	12.5	99629	4	US-09-596-002-37	Sequence 37, Appl
42	44	11.4	1284	3	US-09-327-487A-4	Sequence 4, Appli
43	43.4	11.3	1059	4	US-09-902-540-2579	Sequence 2579, Ap
44	43.4	11.3	14342	4	US-09-902-540-1118	Sequence 1118, Ap
45	43	11.2	1281	3	US-09-327-487A-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-09-012-030-1
; Sequence 1, Application US/09012030
; Patent No. 5912169
; GENERAL INFORMATION:
; APPLICANT: SCHMIDT, Ralf-Michael, STITT, Marc, SONNEWALD,
; APPLICANT: Uwe
; TITLE OF INVENTION: Transketolase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Keil & Weinkeuf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012, 030
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/590,454
; FILING DATE: 22-JAN-1996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2629 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana
; FEATURE:
; NAME/KEY: CDA
; LOCATION: 60..2289
; US-09-012-030-1

Query Match 44.3%; Score 170.4; DB 2; Length 2629;
Best Local Similarity 67.4%; Pred. No. 3e-39;
Matches 240; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

4 CCAGGACCAAGCTGACATCATTTGGGTGGGCGACCGGCTCGAGCTGAGATCGGGGCA 63
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Db 1936 CTGGCAACAACTGATGATCTTTGATTTGGTACTGCTCAGAGTTAGAAATGCTGTC 1995

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QY 64 TTGCGGCGGACAGCTGAGGAAAGAGGGGAAACAGTCCGCGTCTGTCGTTCCTCT 123

Db 1996 AGCGTCGTGATGAACTCAGGAAAGAAAGAAACGATGAGATTGTTCCCTTTGTTT 205

QY 124 GGGAACTCTTTGATGAGCAGTTCGATGAGTACAAAGAGAGCGTCTCTCCGCGCATCA 183

Db 2056 GGGACCTTTTGGAAACAAATCAGCGCATCAACAAAGAAAGTGTCTTCATCATCTGTTA 2115

QY 184 CAGCAGAGATCAGCATTCAGAGCGCGGGTCCACTCTGGCTGGCGAAGTACGTCCGAGGCC 243

Db 2116 CAGCTAGAGTTAGCATTTGAGGCCGCGATCCAATTGGGTTGGAGAAATATGTCGATCAA 2175

QY 244 AAGCAGAGGCCATTGGCATTCGACAAAGTTCCGCGCGCAGTGTCTCTCCGCGAGATCTCA 303

Db 2176 AGGGAAAGCCCATCGGAATTACACATGGGGTGGCCAGTGCCTCTGGAAAAATATACA 2235

QY 304 AGGAGTACGCATCACCGTGGAGAGCATCATTTGCAACTGCCAAGCCTTTAAAG 359

Db 2236 AGGAGTACCGAATTAACGACAGAGCGGTGTGTATGCTGACGCTTAAACAGATTCTTAG 2291

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RESULT 2
US-08-590-454-1
; Sequence 1, Application US/08590454
; Patent No. 5925535
; GENERAL INFORMATION:
; APPLICANT: SCHMIDT, Ralf-Michael, STITT, Marc, SONNEMALD,
; APPLICANT: Use
; TITLE OF INVENTION: Transketolase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinlauf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,454
; FILING DATE: 22-JAN-1996
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2629 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana
; FEATURE:
; NAME/KEY: CDA
; LOCATION: 60..2289
; US-08-590-454-1

Query Match 44.3%; Score 170.4; DB 2; Length 2629;
Best Local Similarity 67.4%; Pred. No. 3e-39;
Matches 240; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 4 CCGGACCAAGCCGATCATCTTGGCTTGGGACCGGCTCCGAGCTGAGATCGCGGACA 63
Db 1936 CTGGCAACAAACCTGATGTCATTTTGATTGGTACTGCTCAGAGTGAATTCCTGCA 123
QY 64 ATGCGCCGACGAGCTGAGGAGGAGGAGGAGGAGCGTCCGGGTGCTCCGTCTCTCT 123
Db 1996 AGCGCTGTGATGAACTCAGGAAAGAGGAAAGAGGAGGAGTGAAGTGTTTCTTTTGT 2055

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QY 124 GGGAACTCTTTGATGAGCAGTCGGATAGTACAAGAGAGAGCGTCTCTCCCTCCGACGTCA 183

Db 2056 GGGAGCTTTTGAAGAACATACCCGACTTACAAAGAAAGTGCTCTTCATCATCTGTTA 2115

QY 184 CAGCGAGATCAGCATCGAGCCCGGCTCACTCGGCTGGCAGAAATATCGTGGAGCC 243

Db 2116 CAGCTAGATTAGCATTTGAGGCGGATTCACATTTGGGTGGAGAAATATGTCCGATCA 2175

QY 244 AAGCCAAAGCCATTGGCATGACAAAGTTGGGCGCGAGTCTCTTGCCGGGACGATCTACA 303

Db 2176 AAGGGAAGGGCCATTCGAAATTGACAGAGGGGTGCGAATGCCCTCGTCAAAAATATACA 2235

QY 304 AGGAGTACGGCATCACCGTGGAGAGCATCAATGCAATGGCAGACAGACTTTTAAG 359

Db 2236 AGGAGTACGGAAATTACACGACAGAGCGCTGTTAGTGCAGTTAAACAAGTTTCTTAA 2291

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RESULT 3
US-09-252-991A-3308
; Sequence 3308, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196, 136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3308
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-3308

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Query Match	30.2%	Score 116.21	DB 4	Length 2007
Best Local Similarity	59.1%	Pred. No. 1.2e-23		
Matches 199	Conservative 0	Mismatches 138	Indels 0	Gaps 0
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Db	589	CGAGCGGAACTGATCTCGATCGCACCGCTTCGGAAATCGGCTCGCGCGAGCCTTA	648	
QY	71	CGACGAGCTAGGAAAGGAGGAAAGCCGTCGCGTCGTCTCGTTCTCTCTGGAACT	130	
Db	649	CGACAAAGCTCGCCAGCAGCGGCCCAAGAGTCGCGGTGGTATCGATGCCATGACACAGCGT	708	
QY	131	CTTTGATGAGCAGTCGGATGAGTACAAAGAGAGGTCCTCTCTGCGACGTCACAGCGAG	190	
Db	709	CTTAAGACAGCAGGACGAGTCTTAAAGACATCTCGTGTGCGGTGAGAAAGTCGCGCGCG	768	
QY	191	GATCAGCATCGAGGCCGAGTCACTCTCGGTGACAGAGTACGTCGAGGCCAAGCGAA	250	
Db	769	CATCGCATCGAGGCCGCCCATGCGCCACTACTGTATCAAGTACGTTGCTTCGACGGGCG	828	
QY	251	GGCATTGGCATCGACAAAGTTCCGCGCGAGTCTCTCGCGGAGCAGATCAAGAGAGTA	310	
Db	829	CATCATCGGATGACACGACTTCGGCGAGTCCGCGCGGCCGCCCGCGCTGTTTCGAGCACTT	888	
QY	311	CGGATCAACCGTGGAGAGCATCAATTGCACATGCCAAG	347	
Db	889	CGGCTTACCTTGACAAAGTCTCTGGCGGTAGCCGAG	925	

RESULT 4
US-09-252-991A-3240
; Sequence 3240, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3240
LENGTH: 2229
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3240

Query Match 30.2%; Score 116.2; DB 4; Length 2229;
Best Local Similarity 59.1%; Pred. No. 1.3e-23;
Matches 199; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

Db 11 CAAGCTGATCATATTGGTTGGGACCGGGCTCGAGCTGAGATCGCGGGCAATGCCG 70
1875 CGAGCCGGAAGTCTGATCTGATCGCCACCGGTTGGAAGTCCGGCTGGCGAGCCCTA 1934
QY 71 CGACGAGCTGAG 130
Db 1935 CGACGAGCTGAG 1994
QY 131 CTTTATGAGCAGTGGATGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 190
Db 1995 CTACGAGCAGCAG 2054
QY 191 GATCAGCATGAG 250
Db 2055 CATGCCATCGAG 2114
QY 251 GGCATTGGCATGACAAAGTTGGCGCGAGAGTCTCTGCGGAGAGATGACAGAG 310
Db 2115 CATCATCGGATGACAGAGCTTGGCGAGAGTGGGCGCGCGCGCGCTGTTGAGAG 2174
QY 311 CGGATCATCCGTGAGAGAGATGATGCAACTGCCAAG 347
Db 2175 CGGCTTACCTTGACAAAGTCTGGCGGTAGCCGAG 2211

QY

RESULT 5
US-09-252-991A-3326/c
Sequence 3326, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3326
LENGTH: 2709
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3326

Query Match 30.2%; Score 116.2; DB 4; Length 2709;
Best Local Similarity 59.1%; Pred. No. 1.4e-23;
Matches 199; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 11 CAAGCTGATCATATTGGTTGGGACCGGGCTCGAGCTGAGATCGCGGGCAATGCCG 70
Db 976 CGAGCCGGAAGTCTGATCTGATCGCCACCGGTTGGAAGTCCGGCTGGCGAGCCCTA 917
QY 71 CGACGAGCTGAG 130
Db 916 CGACGAGCTGAG 857
QY 131 CTTTATGAGCAGTGGATGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 190
Db 856 CTACGAGCAGCAGAGAGAGTCTTACAGAGAGTCCGTGTCGCGGTGGAAGTGGCGCG 797
QY 191 GATCAGCATGAG 250
Db 796 CATGCCATCGAG 737
QY 251 GGCATTGGCATGACAAAGTTGGCGCGAGAGTCTCTGCGGAGAGATGACAGAG 310
Db 736 CATCATCGGATGACAGAGCTTGGCGAGAGTGGGCGCGCGCGCTGTTGAGAGACTT 677
QY 311 CGGATCATCCGTGAGAGAGATGATGCAACTGCCAAG 347
Db 676 CGGCTTACCTTGACAAAGTCTGGCGGTAGCCGAG 640

RESULT 6
US-09-382-106-1
Sequence 1, Application US/09382106
Patent No. 6221631
GENERAL INFORMATION:
APPLICANT: Huang, Jianzhong
APPLICANT: Jiang, Xinh
APPLICANT: McDevitt, Damien
APPLICANT: Van Horn, Stephanie
TITLE OF INVENTION: tkra
FILE REFERENCE: GM10236
CURRENT APPLICATION NUMBER: US/09/382,106
CURRENT FILING DATE: 1999-08-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1998
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-382-106-1

Query Match 29.8%; Score 114.6; DB 3; Length 1998;
Best Local Similarity 58.8%; Pred. No. 3.5e-23;
Matches 198; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 11 CAAGCTGATCATATTGGTTGGGACCGGGCTCGAGCTGAGATCGCGGGCAATGCCG 70
Db 1644 CGAGCCGGAAGTCTGATCTGATCGCCACCGGTTGGAAGTCCGGCTGGCGAGCCCTA 1703
QY 71 CGACGAGCTGAG 130
Db 1704 CGACGAGCTGAG 1763
QY 131 CTTTATGAGCAGTGGATGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 190
Db 1764 CTACGAGCAGCAGAGAGTCTTACAGAGAGTCCGTGTCGCGGTGGAAGTGGCGCG 1823
QY 191 GATCAGCATGAG 250
Db 1824 CATGCCATCGAG 1883
QY 251 GGCATTGGCATGACAAAGTTGGCGCGAGAGTCTCTGCGGAGAGATGACAGAG 310
Db 1884 CATCATCGGATGACAGAGCTTGGCGAGAGTGGGCGCGCGCGCTGTTGAGAGACTT 1943
QY 311 CGGATCATCCGTGAGAGAGATGATGCAACTGCCAAG 347
Db 1944 CGGCTTACCTTGACAAAGTCTGGCGGTAGCCGAG 1980

RESULT 7
US-09-489-039A-1895
; Sequence 1895, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1895
; LENGTH: 2085
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1895

Query Match 27.6%; Score 106.2; DB 4; Length 2085;
Best Local Similarity 56.9%; Pred. No. 9,6e-21;
Matches 195; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 4 CCGGCAACCAAGCTGACATCATTTGGTGGCAACCGGCTCCGAGCTGGAGATCGCGGCA 63
DB 1724 CCGGCGGCAAGCCCGACCTGATCTCTATCGCCACCGGCTGGAGTGGAGATCCGTC 1783
QY 64 ATCCGCGCGACGAGCTGAGAGAGAGGAGAGAGCGGTCCGCTGCTCTGTTCTCTCT 123
DB 1784 TGGCCCGGAAAAAAGTGTGGCCAAAGGGGTAAATGTGGGGGTGCTCGCTCCCTTCA 1843
QY 124 GGGAACTCTTGTATGAGAGTGGATGATGATGATGATGATGATGATGATGATGATGAT 183
DB 1844 CTGATGTGTTGACCGCCGAGATGAGGCGCTCGCGCAATCGGTGCTGCGTGGACGTCA 1903
QY 184 CAGCGAGATCAGCATCAGAGCGCGGTGCTCACTCTCGGCTGGAGAGTACGTGGAGCCC 243
DB 1904 GCGCCCGGCTGGCGGTGCGAAGCCGGATAGCGGATGATGATGATGATGATGATGAT 1963
QY 244 AAGGCAAGGCAATGGCATGACAAATTTGGCGCGAGTCTCTCGCGGAGCATCTACA 303
DB 1964 AAGGCAAGATCGTGGCATGACCGGCTATGGCAATCCCGCGGAGAGCAGTTGTTCC 2023
QY 304 AAGATACCGCATCAGCGGTGAGAGCATGATGCAACTGCCAA 346
DB 2024 CGTTCTTTGGCTTTACGATCGATCATATGCTGCCACCGCGCA 2066

RESULT 8
US-09-489-039A-4813
; Sequence 4813, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4813
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4813

Query Match 26.1%; Score 100.4; DB 4; Length 2127;
Best Local Similarity 55.8%; Pred. No. 4.6e-19;

Matches 191; Conservative 0; Mismatches 151; Indels 0; Gaps 0;
QY 5 CCGCACCAGCCGTCATCATGTTGGTGGCAACCGGCTCCGAGCTGGAGATCGCGGCA 64
DB 1773 CGCCGGCCAGCCGAGCTGATCTTATCGCCACCGGTTCAAGAGTGGAGCTGGCTTGC 1832
QY 65 TGGCGCCGACGAGCTGAG 124
DB 1833 CGCATGGACCAATGACCTGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1892
QY 125 GGAATCTTTATGAGCACTCGATGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAG 184
DB 1893 CAGCGGTTGCAAGAGAGAGATCGCGCTTATCGCAATCCGATCGAGAGAGAGAG 1952
QY 185 ACCGAGATCAGCATCAGAGCGCGGTGCACTCTCGGCTGGAGAGTACGTCGAGCCCA 244
DB 1953 CGCGCGCTTGGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2012
QY 245 AAGCAAGCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304
DB 2013 CGCGCTATCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2072
QY 305 GGAGTACCGCATCAGCGGTGAGAGAGATGATGCAACTGCCAA 346
DB 2073 GGAGTTCGCTTACCGGTTGATGATGATGATGATGATGATGATGATGATGATGAT 2114

RESULT 9
US-08-311-731A-127
; Sequence 127, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P. C.
; CITY: BOSTON
; STREET: 600 ATLANTIC AVENUE
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 127:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35881 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LAPRAE
US-08-311-731A-127

Query Match 25.7%; Score 99; DB 4; Length 35881;
Best Local Similarity 56.2%; Pred. No. 3.6e-18;
Matches 186; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 13 ACCTGACATCATTTGGGTTGGGCAACCGCTCCGAGCTGAGATCGCGGCAATGCGCGG 72
DB 19067 AGCTGACATCATTTGATGTCGACCGGATCGAGGTCCAACTCGTGTGCGAGCTCAGA 19126
QY 73 ACAGCTGAGAGAGAGGAG 132
DB 19127 AGTTGTGGCGGATTAAGACATCATTTGTGCGGGTGTGTGATGCGGTGTGGAATGAT 19186
QY 133 TTGATAGAGAGTCGATGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 192
DB 19187 TCGAGTCAAGCGCGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 19246
QY 193 TCAGCATCGAGGCGCGGCTCACTCTCGGCTGGGAGAGATGATGATGATGATGATGATGAT 252
DB 19247 TGGCCCTCGAGGCGCGGCTCGGCTGATGATGATGATGATGATGATGATGATGATGAT 19306
QY 253 CCATTGGCATGACAAATTCGCGGCGAGTCTCTCGGCGGAGATCTACAAAGAGATGAG 312
DB 19307 TTGTGTCATCGAGCACTACGCGGAGATTCGAGATTAACAGACTTTGTTCCGTGATGAG 19366
QY 313 GCATCACCGTGGAGAGACATTCGCACTGC 343
DB 19367 GCTTACGCGGAGGCGGTGTTGCCGAGC 19397

RESULT 10

US-09-531-266-1
Sequence 1, Application US/09531266
Patent No. 6797509
GENERAL INFORMATION:
APPLICANT: DUNICAN, L.K.
APPLICANT: MCCORMACK, ASHLING
APPLICANT: STAPELTON, CLIONA
APPLICANT: BURKE, KEVIN
APPLICANT: MCKEL, BETTINA
TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE TAL GENE
FILE REFERENCE: MAS/21123/258100
CURRENT APPLICATION NUMBER: US/09/531,266
CURRENT FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/142,915
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 6995
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (2471)..(3550)
OTHER INFORMATION: tal-Gen
US-09-531-266-1

Query Match 24.4%; Score 93.8; DB 4; Length 6995;
Best Local Similarity 54.9%; Pred. No. 5.9e-17;
Matches 185; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY 15 CCTGACATCATTTGGGTTGGGCAACCGCTCCGAGCTGAGATCGCGGCAATGCGCGCAGC 74
DB 1953 CCAGATGATCTCTCATTTGGGCTCCGCTCCGAGGTTCAAGTTTAACGCTGCGAAG 2012
QY 75 GAGCTGAG 134
DB 2013 GCTCTGAAAGCTGAGGCGCTTGCAGCTCGGTTGTTTCGTTCCATTGATGATGATGATG 2072
QY 135 GATGAGACATCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 194
DB 2073 CAGGAGCAG 2132

QY 195 AGCATGAGAGCGCGGCTCCACTCTCGGCTGGGAGAGTACGTGAGAGAGAGAGAGAGAG 254
DB 2133 TCTGTTGAAGCTGGGATGCGAAATGCTTGTGATCCCTTCTTGGGACCCAGGCGGTGT 2192
QY 255 ATTGACATGAGAGAGTTCGCGCGGAGTGTCTCTCGGCGGAGCATCTACAAAGATGAGC 314
DB 2193 GTCTCCCTTGACACTTCGCTGCTCTCTGAGATTAACAGACCTCTGTTAGAGAGTTCG 2252
QY 315 ATCACCCTGAGAGAGATCATTTGCAACTGCGCAAGACT 351
DB 2253 ATCACCACCGATGAGTGTGCGACGCGGCAAGACT 2289

RESULT 11

US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match 22.3%; Score 85.8; DB 3; Length 4403765;
Best Local Similarity 53.0%; Pred. No. 1.6e-13;
Matches 183; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 2 AACCGGACCAAGCCTGACATCATTTGGGTTGGGCAACCGCTCCGAGCTGAGATGCGGG 61
DB 1628319 ACCGGGCGAGGAACCGACGTCATTCATGCGCACCGGCTCGAGGTGCACTGCGGGT 1628260
QY 62 CAATGCGGCGGAGAGCTGAG 121
DB 1628259 CGCGGCGGAGAGCTTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1628200
QY 122 CTGGGAATCTTTGATGAG 181
DB 1628199 CCGTGAAGTGTTCGAGGCGGACCACTTACAGAGTACCGGCGGAGTGTGCGGAG 1628140
QY 182 CACAGCAGAGATCAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241
DB 1628139 GTGCGGCGGAGTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1628080
QY 242 CCAAGGCAAGGCGCATTTGGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
DB 1628079 CACGGGCGGAGTGTGCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1628020
QY 302 CAAGAGTACGAGCATCACCGGTGAGAGAGATCATTTGCAACTGCGCA 346
DB 1628019 CCGCAGTACGAGCTTCACTGCGGAGGCGGTGCGGCGGCGGCGGCGGCGGCGG 1627975

RESULT 12

US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328

✓

OPERATING SYSTEM: WINDOWS 95

SOFTWARE: Word Perfect 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,693A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: W. Gary Goodson
REGISTRATION NUMBER: 22,387
REFERENCE/DOCKET NUMBER: Lit-Pi-296
TELECOMMUNICATION INFORMATION:
TELEPHONE: (208)526-8339
TELEFAX: (208)526-8339
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 6641 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-064-693A-25

Query Match 21.5%; Score 82.8; DB 3; Length 6641;
Best Local Similarity 53.0%; Pred. No. 8,7e-14;
Matches 177; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 13 AGCTGACATCATTTGGTGGGACCGGCTCCGAGCTGAGATCGCGGCAATGCGCGG 72
DB 3768 ACCCGAATGATTTTCATCGCTACCGGTTCAAGATTAAGTGGTGTGCTGCTACG 3827
QY 73 AGGAGTGGAG 132
DB 3828 AAAAATGATCTCCGAAAGCGTAAAGCGCGGTGTGTGTCATGTCTTACCGAGCAT 3887
QY 133 TTGATGAGAGATCGGATGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 192
DB 3888 TTGACAGAGAGATGCTGCTTACCGTAAATCCGTAAGTACGCGGTTACTGACGCG 3947
QY 193 TCAGATCGAGGCGCGGTCACCTCTCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
DB 3948 TTGCTGTAGAGAGCGGGTATTTGCTGACTTGTGTAAGATATTTGGCCCTGAAGGTCGA 4007
QY 253 CCATTGGCATCACAAGTTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 312
DB 4008 TCGTGTGATGACCACTTCGCTGATCTGCTCGGAGAGAGAGAGAGAGAGAGAGAG 4067
QY 313 GCATCAGCGTGGAG 346
DB 4068 GCTTCACTGTGTATTAAGTTGTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4101

RESULT 15
US-08-961-527-49
Sequence 49, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 11443 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-49

Query Match 20.9%; Score 80.6; DB 3; Length 11443;
Best Local Similarity 51.9%; Pred. No. 4,7e-13;
Matches 182; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 17 TGACATCATTTGGGTTGGGACCGGCTCCGAGCTGAGAGATCGCGGCAATGCGCGGAGAGCA 76
DB 10003 TGATCATTTATCATTTGCTACAGAGATCTGAGGTCAATCTAGCTATCAAGCTGCTAAGCA 10062
QY 77 GCTGAG 136
DB 10063 ATTGGTTTACAGGTGTAAGTACGTGTGTATCTATGCTTACCGCTTACCGAGAGATTTTGA 10122
QY 137 TGAGAGTCGATGATGATCAAG 196
DB 10123 TGCTCAAGATGTACTCTCAAG 10182
QY 197 CATGAGGCGGGTCACTCTCGCTGCGAGAGATGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 256
DB 10183 CATGAAATGAG 10242
QY 257 TGGCATGCAAGTTCGGGCGAGAGTCTCTCGCGGAGAGATCTCAAGAGAGATGAGAGAGAT 316
DB 10243 CGGTATTACATCTTGGGTGCTTGGCCAGCTGAGCTGATGATTAATTAATTAATTAATTAAT 10302
QY 317 CACCGTGAAGAGATCATTTGCACTGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
DB 10303 TACGTTAGAGATATCTGTTGCTCAAGTTAAGTCCCTATAGAGAGAGAGAGAGAGAGAGAG 10353

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Job time: 126.658 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: May 4, 2005, 12:06:42 ; Search time 436.803 Seconds
(without alignments)
5365.716 Million cell updates/sec

Title: US-09-300-482-356

Perfect score: 385
Sequence: 1 CAACCGGCAACCAAGCTGAC.....ACGCTGAGGAGTCTTTT 385

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	385	100.0	385	US-09-987-899-4513	Sequence 4513, Ap
2	363.2	94.3	1656	US-10-425-114-609	Sequence 609, App
3	361	93.8	1420	US-10-425-114-19700	Sequence 19700, A
4	359.4	93.4	3311	US-10-425-115-157267	Sequence 157267, A
5	356.8	92.7	1686	US-10-425-114-3351	Sequence 3351, Ap
6	326.8	86.9	423	US-09-987-899-4512	Sequence 4512, Ap
7	295.2	76.7	300	US-09-987-899-4502	Sequence 4502, Ap
8	292.2	75.9	2107	US-10-767-701-14710	Sequence 14710, A
9	265	64.8	273	US-09-987-899-4499	Sequence 4499, Ap
10	249.6	64.8	276	US-09-987-899-4501	Sequence 4501, Ap
11	247.8	64.4	646	US-10-333-184-131	Sequence 131, App

12	247.8	64.4	1122	17	US-10-333-184-361	Sequence 361, App
13	247.6	64.3	2636	18	US-10-437-963-84321	Sequence 84321, A
14	247.6	64.3	630	18	US-10-767-701-10148	Sequence 10148, A
15	246.4	64.0	2869	18	US-10-739-930-5298	Sequence 5298, A
16	245	63.6	1127	17	US-10-333-184-156	Sequence 156, App
17	241.2	62.6	299	11	US-09-987-899-4504	Sequence 4504, Ap
18	232	60.3	630	9	US-09-910-664-118	Sequence 118, App
19	232	60.3	630	17	US-10-333-184-138	Sequence 138, App
20	230.4	59.8	622	17	US-10-333-184-139	Sequence 139, App
21	211	54.8	649	18	US-10-425-115-153110	Sequence 153110, A
22	209.2	54.3	242	11	US-09-987-899-4505	Sequence 4505, Ap
23	189.4	49.2	235	11	US-09-987-899-4477	Sequence 4477, Ap
24	183.8	47.7	1758	17	US-10-260-238-9497	Sequence 5947, Ap
25	183.8	47.7	2354	18	US-10-437-963-88892	Sequence 88892, A
26	178.8	46.4	1146	17	US-10-424-559-32349	Sequence 32349, A
27	176.6	45.9	630	18	US-10-767-701-3173	Sequence 3173, A
28	171.6	44.6	978	17	US-10-425-114-9690	Sequence 9690, Ap
29	171.6	44.6	2168	17	US-10-425-114-9339	Sequence 9339, Ap
30	171.6	44.6	3914	17	US-10-424-559-96112	Sequence 96112, A
31	168.8	43.8	2594	17	US-10-333-184-334	Sequence 334, App
32	164.8	42.8	265	11	US-09-987-899-4507	Sequence 4507, Ap
33	163	42.3	1172	9	US-09-910-664-121	Sequence 121, App
34	163	42.3	1239	17	US-10-333-184-135	Sequence 135, App
35	163	42.3	693	17	US-10-333-184-168	Sequence 168, App
36	162.8	42.3	15172	17	US-10-380-935-32	Sequence 32, App1
37	161.8	42.0	15172	17	US-10-380-935-36	Sequence 36, App1
38	161.4	41.9	2608	17	US-10-333-184-129	Sequence 129, App
39	161.4	41.9	647	17	US-10-333-184-129	Sequence 129, App
40	160.8	41.8	693	17	US-10-333-184-200	Sequence 200, App
41	160.8	41.8	581	9	US-09-770-152-150	Sequence 150, App
42	155	40.3	2226	9	US-09-938-842A-283	Sequence 283, App
43	155	40.3	2226	11	US-09-938-842A-283	Sequence 283, App
44	155	40.3	2226	11	US-09-938-842A-283	Sequence 283, App
45	150.8	39.2	287	11	US-09-987-899-4506	Sequence 4506, Ap

ALIGNMENTS

RESULT 1
US-09-987-899-4513
Sequence 4513, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4513
LENGTH: 385
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3078-007-Q1-X1-G3
US-09-987-899-4513

Query Match 100.0%, Score 385, DB 11, Length 385;
Best local Similarity 100.0%, Pred. No. 1.8e-108;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CAACCGGCAACCAAGCTGACATTCATTTGGTTGGGACCGGCTCCAGTGTGAGATCGCGG 60
1 CAACCGGCAACCAAGCTGACATTCATTTGGTTGGGACCGGCTCCAGTGTGAGATCGCGG 60

QY 61 GCAATGCGCGCGAGAGCTGAGAGAGAGGAGAGAGCGGTCCGCTGCTCTGTTGCTCT 120
|
|
|
Db 61 GCAATGCGCGCGAGAGCTGAGAGAGAGGAGAGAGCGGTCCGCTGCTCTGTTGCTCT 120
|
|
|
QY 121 CTTGGGAACCTTTTATGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGCGAGC 180
|
|
|
Db 121 CTTGGGAACCTTTTATGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGCGAGC 180
|
|
|
QY 181 TCACAGGAGAGATGACATCGAGCGCGGCTCCTCTCGGCTGGCAGAGTACGTCGAG 240
|
|
|
Db 181 TCACAGGAGAGATGACATCGAGCGCGGCTCCTCTCGGCTGGCAGAGTACGTCGAG 240
|
|
|
QY 241 CCCAAGGCAAGGCGCATTCGATCGACAAGTTCCGCGGAGAGTCCCTCCGCGAGCATCT 300
|
|
|
Db 241 CCCAAGGCAAGGCGCATTCGATCGACAAGTTCCGCGGAGAGTCCCTCCGCGAGCATCT 300
|
|
|
QY 301 ACAAGAGATACCGCATCACCGTGGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 360
|
|
|
Db 301 ACAAGAGATACCGCATCACCGTGGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 360
|
|
|
QY 361 TAACAACGCTCTGGAGATTTTTTT 385
|
|
|
Db 361 TAACAACGCTCTGGAGATTTTTTT 385
|
|
|

RESULT 2
US-10-425-114-609
; Sequence 609, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 609
; LENGTH: 1656
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700084322_FLI
US-10-425-114-609

Query Match 94.3%; Score 363.2; DB 17; Length 1656;
Best Local Similarity 96.6%; Pred. No. 1.2e-101;
Matches 371; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 CAACCGGCAACCAAGCCTGACATCATTTGGTTGGGCAACCGGCTCCGAGCTGAGATCGCG 60
|
|
|
Db 1023 CGACCGGCAACCAAGCCTGACATCATTTGATGAGGAGCAACCGGCTCCGAGCTGAGATCGCG 1082
|
|
|
QY 61 GCAATGCGCGCGAGAGCTGAGAGAGAGGAGAGAGCGTCCGCTCGCTCTGTTGCTCT 120
|
|
|
Db 1083 CCAAGGCGCGCGAGAGCTGAGAGAGAGGAGAGAGCGTCCGCTCGCTCTGTTGCTCT 1142
|
|
|
QY 121 CTTGGGAACCTTTTATGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGCGAGC 180
|
|
|
Db 1143 CTTGGGAACCTTTTATGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGCGAGC 1202
|
|
|
QY 181 TCACAGGAGAGATGACATCGAGCGCGGCTCCTCTCGGCTGGCAGAGTACGTCGAG 240
|
|
|
Db 1203 TCACAGGAGAGATGACATCGAGCGCGGCTCCTCTCGGCTGGCAGAGTACGTCGAG 1262
|
|
|
QY 241 CCCAAGGCAAGGCGCATTCGATCGACAAGTTCCGCGGAGAGTCCCTCCGCGAGCATCT 300
|
|
|

Db 1263 CCCAAGGCAAGGCGCATTCGATCGACAAGTTCCGCGGAGAGTCCCTCCGCGAGCATCT 1322
|
|
|
QY 301 ACAAGAGATACCGCATCACCGTGGAGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 360
|
|
|
Db 1323 ACAAGAGATACCGCATCACCGTGGAGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 1382
|
|
|
QY 361 TAACAACGCTCTGGAGATTTTTTT 384
|
|
|
Db 1383 TAACAACGCTCTGGAGATTTTTTT 1406
|
|
|

RESULT 3
US-10-425-114-19700
; Sequence 19700, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19700
; LENGTH: 1420
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-102-F10_FLI
US-10-425-114-19700

Query Match 93.8%; Score 361; DB 17; Length 1420;
Best Local Similarity 96.1%; Pred. No. 5.5e-101;
Matches 370; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1 CAACCGGCAACCAAGCCTGACATCATTTGGTTGGGCAACCGGCTCCGAGCTGAGATCGCG 60
|
|
|
Db 790 CGACCGGCAACCAAGCCTGACATCATTTGATGAGGAGCAACCGGCTCCGAGCTGAGATCGCG 849
|
|
|
QY 61 GCAATGCGCGCGAGAGCTGAGAGAGAGGAGAGAGCGTCCGCTCGCTCTGTTGCTCT 120
|
|
|
Db 850 CCAAGGCGCGCGAGAGCTGAGAGAGAGGAGAGAGCGTCCGCTCGCTCTGTTGCTCT 909
|
|
|
QY 121 CTTGGGAACCTTTTATGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGCGAGC 180
|
|
|
Db 910 CTTGGGAACCTTTTATGATGAGCAGTCCGATGAGTCAAGAGAGAGCGTCCCTCCGCGAGC 969
|
|
|
QY 181 TCACAGGAGAGATGACATCGAGCGCGGCTCCTCTCGGCTGGCAGAGTACGTCGAG 240
|
|
|
Db 970 TCACAGGAGAGATGACATCGAGCGCGGCTCCTCTCGGCTGGCAGAGTACGTCGAG 1029
|
|
|
QY 241 CCCAAGGCAAGGCGCATTCGATCGACAAGTTCCGCGGAGAGTCCCTCCGCGAGCATCT 300
|
|
|
Db 1030 CCCAAGGCAAGGCGCATTCGATCGACAAGTTCCGCGGAGAGTCCCTCCGCGAGCATCT 1089
|
|
|
QY 301 ACAAGAGATACCGCATCACCGTGGAGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 360
|
|
|
Db 1090 ACAAGAGATACCGCATCACCGTGGAGAGAGCATTCATTGCACTGCCAAGAGCTTTTAAGAGC 1149
|
|
|
QY 361 TAACAACGCTCTGGAGATTTTTTT 385
|
|
|
Db 1150 TAACAACGCTCTGGAGATTTTTTT 1174
|
|
|

RESULT 4
US-10-425-115-157267
; Sequence 157267, Application US/10425115
; Publication No. US20040214272A1

```

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
LENGTH: 3311
TYPE: DNA
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: MRT4577_75006C.1
US-10-425-115-157267

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Query Match      93.4%; Score 359.4; DB 18; Length 3311;
Best Local Similarity 95.8%; Pred. No. 2e-100;
Matches 369; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 CAACCGGACCAAGCCTGACATCTGGGTCACCGGCTCCGAGCTGAGATCGCG 60
DB 2233 CGACCGGCAACAGCCTGACCTGATGTGATGGGACCGGCTCCGAGCTGAGATCGCG 2292
QY 61 GCAATCGGCGCCGACGAGCTGAGGAGGAGGAGGAGCGGCTCGGCTGCTGCTGCT 120
DB 2293 CCAAGGCGCCGACGAGCTGAGGAGGAGGAGGAGCGGCTCGGCTGCTGCTGCT 2352
QY 121 CCGGGAACCTTTGATGAGCAGTGGATGAGTCAAGAGAGAGCGTCTCCCTGCGGAG 180
DB 2353 CCGGGAACCTTTGATGAGCAGTGGATGAGTCAAGAGAGAGCGTCTCCCTGCGGAG 2412
QY 181 TCACAGCGAGATCAGCATCGAGGCGGGTCCACTCTCGGCTGAGAGTACGTGAG 240
DB 2413 TCACAGCGAGATCAGCATCGAGGCGGGTCCACTCTCGGCTGAGAGTACGTGAG 2472
QY 241 CCCAAGGCAAGGCGCATTTGGCATGACAGTTCGGCGGAGTCTCTGCGGAGCATCT 300
DB 2473 CCCAAGGCAAGGCGCATTTGGCATGACAGTTCGGCGGAGTCTCTGCGGAGCATCT 2532
QY 301 ACAAGGAGTACCGGATCAGCGTGGAGAGCATCTTTCACCTGCGAAGAGCTTTAAGAC 360
DB 2533 ACAAGGAGTACCGGATCAGCGTGGAGAGCATCTTTCACCTGCGAAGAGCTTTAAGAC 2592
QY 361 TAACAACGGCTCGGAGATTTTTTTT 385
DB 2593 TAACAACGGCTCGGAGATTTTTTTT 2617

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RESULT 5
US-10-425-114-3351
Sequence 3351, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaka, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 3351
LENGTH: 1686
TYPE: DNA
ORGANISM: Zea mays

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FEATURE:
OTHER INFORMATION: Clone ID: 700262031_FLI
US-10-425-114-3351

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Query Match      92.7%; Score 356.8; DB 17; Length 1686;
Best Local Similarity 95.6%; Pred. No. 1.1e-99;
Matches 367; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 CAACCGGACCAAGCCTGACATCTTTGGTGGGACCGGCTCCGAGCTGAGATCGCG 60
DB 1119 CGACCGGCAACAGCCTGACCTGATGTGATGGGACCGGCTCCGAGCTGAGATCGCG 1178
QY 61 GCAATCGGCGCCGACGAGCTGAGGAGGAGGAGGAGCGGCTCGGCTGCTGCTGCT 120
DB 1179 CCAAGGCGCCGACGAGCTGAGGAGGAGGAGGAGCGGCTCGGCTGCTGCTGCT 1238
QY 121 CCGGGAACCTTTGATGAGCAGTGGATGAGTCAAGAGAGCGTCTCCCTGCGGAG 180
DB 1239 CCGGGAACCTTTGATGAGCAGTGGATGAGTCAAGAGAGCGTCTCCCTGCGGAG 1298
QY 181 TCACAGCGAGATCAGCATCGAGGCGGGTCCACTCTCGGCTGAGAGTACGTGAG 240
DB 1299 TCACAGCGAGATCAGCATCGAGGCGGGTCCACTCTCGGCTGAGAGTACGTGAG 1358
QY 241 CCCAAGGCAAGGCGCATTTGGCATGACAGTTCGGCGGAGTCTCTGCGGAGCATCT 300
DB 1359 CCCAAGGCAAGGCGCATTTGGCATGACAGTTCGGCGGAGTCTCTGCGGAGCATCT 1418
QY 301 ACAAGGAGTACCGGATCAGCGTGGAGAGCATCTTTCACCTGCGAAGAGCTTTAAGAC 360
DB 1419 ACAAGGAGTACCGGATCAGCGTGGAGAGCATCTTTCACCTGCGAAGAGCTTTAAGAC 1478
QY 361 TAACAACGGCTCGGAGATTTTTTTT 384
DB 1479 TAACAACGGCTCGGAGATTTTTTTT 1502

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RESULT 6
US-09-987-899-4512
Sequence 4512, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jindong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4512
LENGTH: 423
TYPE: DNA
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: LIB3060-013-Q1-K1-A12
US-09-987-899-4512

Query Match      84.9%; Score 326.8; DB 11; Length 423;
Best Local Similarity 95.2%; Pred. No. 1.5e-90;
Matches 337; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 CAACCGGACCAAGCCTGACATCTTTGGTGGGACCGGCTCCGAGCTGAGATCGCG 60
DB 70 CGACCGGCAACAGCCTGACCTGATGTGATGGGACCGGCTCCGAGCTGAGATCGCG 129
QY 61 GCAATCGGCGCCGACGAGCTGAGGAGGAGGAGGAGCGGCTCGGCTGCTGCTGCT 120

```

Db 130 CCAAGCGCCGACGACTGAGAGAGAGGCGCAAGCGCTCCGCTGCTCTGCTCT 189
QY 121 CTTGGGAACTCTTTGATGATGACGATCGGATGATCAAGAGAGCGTCTCTGCCGACG 180
Db 190 CTTGGGAACTCTTTGATGATGACGATCGGATGATCAAGAGAGCGTCTCTGCCGACG 249
QY 181 TCACAGGAGATCAGATCGAGGCGGGGTCCTCTCCGCTGGCAGAACTAGCTGGAG 240
Db 250 TCACAGGAGATCAGATCGAGGCGGGGTCCTCTCCGCTGGCAGAACTAGCTGGAG 309
QY 241 CCCAAGGCAAGCCATTGGCATCGACAACTTCGCGCGAGTGTCTCTGCCGAGCATCT 300
Db 310 CCCAGGGCAAGCCATTGGCATCGACAACTTCGCGCGAGTGTCTCTGCCGAGCATCT 369
QY 301 ACAAGAGTCCGCGATCACTCGTGGAGAGCATCTTGAATCGCAAGACTTTT 354
Db 370 ACAAGAGTACCGCATCACCGTGGAGAGCATCTTGAATCGCAAGACTTT 423

RESULT 7
US-09-987-899-4502

Sequence 4502, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jingdong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4502
LENGTH: 300
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700048347H1
US-09-987-899-4502

Query Match 76.7%; Score 295.2; DB 11; Length 300;
Best Local Similarity 99.0%; Pred. No. 7,9e-81;
Matches 297; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 71 CGACGAGCTGAGGAGAGAGGAGAGCGGTCGCGCTGCTCTGCTGCTCTGAGAACT 130
Db 1 CGACGAGCTGAGGAGAGAGGAGAGCGGTCGCGCTGCTCTGCTGCTCTGAGAACT 60
QY 131 CTTTATGATGACGCTGGATGATGATCAAGAGAGCGTCTCTGCGAGCGTCAACGAG 190
Db 61 CTTTATGATGACGCTGGATGATGATCAAGAGAGCGTCTCTGCGAGCGTCAACGAG 120
QY 191 GATCAGCATCGAGGCGGGTCCACTCTGGCTGGAGAGATCGTCCGAGCCCAAGGCA 250
Db 121 GATCAGCATCGAGGCGGGTCCACTCTGGCTGGAGAGATCGTCCGAGCCCAAGGCA 180
QY 251 GGCATTGGCATCGAAGTTGCGGCGAGTGTCTCTGCGGAGCATCTCAAGAGATA 310
Db 181 GGCATTGGCATCGAAGTTGCGGCGAGTGTCTCTGCGGAGCATCTCAAGAGATA 240
QY 311 CGGCAATCCGTTGGAGAGAGATCATCTGCAATGCCAAGGCTTTTAAGGCTPAACCGT 370
Db 241 CGGCAATCCGTTGGAGAGAGATCATCTGCAATGCCAAGGCTTTTAAGGCTPAACCGT 300

US-10-767-701-14710
Sequence 14710, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5353) B
CURRENT APPLICATION NUMBER: US/10/767,701
PRIOR FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 14710
LENGTH: 2107
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAV03-CLUS7982_1
US-10-767-701-14710

Query Match 75.9%; Score 292.2; DB 18; Length 2107;
Best Local Similarity 84.9%; Pred. No. 9,3e-80;
Matches 327; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 CAACCGGCAACCAAGCTTATCATCTGTTGGGACCGGCTCCGAGCTGAGATCGCG 60
Db 1244 CAATCGGCAACCAAGCTTATCATCTGTTGGGACCGGCTCCGAGATCGAGATTCGCG 1303
QY 61 GCATGCGCGCGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 1304 AAAAGGCTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1363
QY 121 CTTGGAACTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
Db 1364 CTTGGAACTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1423
QY 181 TCACGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
Db 1424 TCACGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1483
QY 241 CCCAAGGCAAGCCATTGGCATCGACAACTTCGCGCGAGTGTCTCTGCGGAGCATCT 300
Db 1484 CCCAAGGCAAGCCATTGGCATCGACAACTTCGCGCGAGTGTCTCTGCGGAGCATCT 1543
QY 301 ACAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 1544 ACAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1603
QY 361 TAACACGCTGCGAGATTTT 385
Db 1604 TAACACACACAGCTTGAATTTT 1628

RESULT 9
US-09-987-899-4499

Sequence 4499, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jingdong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
NUMBER OF SEQ ID NOS: 7341

SEQ ID NO 4499
LENGTH: 273
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 70004475SH1
US-09-987-899-4499

Query Match 68.8%; Score 265; DB 11; Length 273;
Best Local Similarity 98.2%; Pred. No. 1.6e-71;
Matches 268; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 50 GGAGATCCGGGCAATCCGCGCCGACGAGTGTAGAGAAAGGGGAAAGACGGTCCGCTCT 109
DB 1 GGAGATCCGGGCAATCCGCGCCGACGAGTGTAGAGAAAGGGGAAAGACGGTCCGCTCT 60
QY 110 CTCGTTCT 169
DB 61 CTCGTTCT 120
QY 170 CCTCGCCGACGTACAGCAGGAGATCGATCGAGCGCGGCTCCACTCTCTCTCTCTCTCT 229
DB 121 CCTCGCCGACGTACAGCAGGAGATCGATCGAGCGCGGCTCCACTCTCTCTCTCTCTCT 180
QY 230 GTACGTCGAGCGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 289
DB 181 GTACGTCGAGCGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 290 CGGAGCATCTCAAGAGAGTACGCGATCACCGT 322
DB 241 CGGAGCATCTCAAGAGAGTACGCGATCACCGT 273

RESULT 10

US-09-987-899-4501
Sequence 4501, Application US/09987899
Publication No. US20040116682A1
GENERAL INFORMATION:
APPLICANT: Cheikh, Nordin
APPLICANT: Liu, Jingdong
APPLICANT: Miller, Phillip W.
APPLICANT: O Connell, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
FILE REFERENCE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/262,979
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: US 60/076,712
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 7341
SEQ ID NO 4501
LENGTH: 276
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700027425H1
US-09-987-899-4501

Query Match 64.8%; Score 249.6; DB 11; Length 276;
Best Local Similarity 96.4%; Pred. No. 8.7e-67;
Matches 266; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 14 GCGTGCATCATTTGGTGGGACCGGCTCCGAGCTGAGATCGCGGGAATGCGGCGCA 73
DB 1 GCGTGCATCATTTGGTGGGACCGGCTCCGAGCTGAGATCGCGGGAATGCGGCGCA 60
QY 74 CGAGCTGAGG-AAGAGGGGAAAGCGGTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 132
DB 61 CGAGCTGAGGTATGAGGGGAAAGCGGTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 133 TTGATGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 192

DB 121 TTGATGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 193 TCAGCATCAGGCGCGGCTCACTCTCGCTGCGAGAGTACGTCCGAGCCCAAGGCAAG 252
DB 181 TCAGCATCAGGCGCGGCTCACTCTCGCTGCGAGAGTACGTCCGAGCCCAAGGCAAG 240
QY 253 CCATTGGCATCGACAAGTTCCGCGGAGTGTCTCTG 288
DB 241 CCATTGGCATCGACAAGTTCCGCGGAGTGTCTCTG 276

RESULT 11

US-10-333-184-131
Sequence 131, Application US/10333184
Publication No. US20040088762A1
GENERAL INFORMATION:
APPLICANT: Reddy, Avutu
APPLICANT: Larrinua, Ignacio
APPLICANT: Skokut, Thomas
APPLICANT: Smith, Doug
APPLICANT: Hu, Zihua
APPLICANT: Ruegger, Max
APPLICANT: Shukla, Vipula
APPLICANT: Bauer, Teresa
APPLICANT: Weigartz, Ted
APPLICANT: Blakslee, Beth
APPLICANT: Oriedo, Jeremiah
APPLICANT: Savickas, Phillip
APPLICANT: McCreary, David
APPLICANT: Miller, Barbara
APPLICANT: della-Cioppa, Gregory
TITLE OF INVENTION: Nucleic Acid Compositions Conferring Dwarfism Phenotype
FILE REFERENCE: DOW-04681
CURRENT APPLICATION NUMBER: US/10/333,184
PRIOR FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 60/219,809
PRIOR FILING DATE: 2000-07-20
SOFTWARE: Patent in version 3.0
NUMBER OF SEQ ID NOS: 571
SEQ ID NO 131
LENGTH: 646
TYPE: DNA
ORGANISM: Oryza japonica
US-10-333-184-131

Query Match 64.4%; Score 247.8; DB 17; Length 646;
Best Local Similarity 80.2%; Pred. No. 3.6e-66;
Matches 291; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1 CAACCGGACCAAGGCTGACATCATTTGGTGGGACCGGCTCCGAGCTGAGATCGCGG 60
DB 170 CAACCGGACCAAGGCTGACATCATTTGGTGGGACCGGCTCCGAGCTGAGATCGCGG 229
QY 61 GCAATGCGGCGCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 230 CCAAGGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 289
QY 121 CCGGAGACTCTTTATGATGAGTGGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 290 GCTGGAGCTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 349
QY 181 TCACAGCGAGATCAGATCGAGGCGGCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 350 TTAAGTCAAGAGTACGCTTGAAGCAGGCTTAAGTCAAGAGTCAAGAGTCAAGAGTCA 409
QY 241 CCAAGGCAAGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 410 GCAAGGCAAGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
QY 301 ACAAGAGATCAGGATCAGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 470 ACCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529

CURRENT APPLICATION NUMBER: US/10/767,701
 CURRENT FILING DATE: 2004-01-29
 NUMBER OF SEQ ID NOS: 63128
 SEQ ID NO 10148
 LENGTH: 630
 TYPE: DNA
 ORGANISM: Sorghum bicolor
 FEATURE:
 OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS61383_1
 US-10-767-701-10148

Query Match 64.3%; Score 247.6; DB 18; Length 630;
 Best Local Similarity 80.7%; Pred. No. 4,2e-66;
 Matches 289; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 CAACGGGACCAAGCTTGATCATTTGGGTCGACCGGCTCCGAGCTGAGATCGCG 60
 DB 7 CAACGAGCAACAGCTGATCTCATCTGTGTGATACCGGCTCTGAACTAGAGATTGCTG 66
 QY 61 GCAATGCGGCGGACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 DB 67 CCAAGGCTGCTGATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
 QY 121 CTTGGGAATCTTTTGTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 180
 DB 127 CTTGGGAATCTTTTGTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 186
 QY 181 TCACAGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 DB 187 TTACTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 246
 QY 241 CCCAAGGCAAGGCTTGGCATGCAAGTTCGGCGGAGTCTCTGCGGAGAGATCT 300
 DB 247 CCCAAGGCAAGGCTTGGCATGCAAGTTCGGCGGAGTCTCTGCGGAGAGATCT 306
 QY 301 ACAAGAGTACGGCATCAACCGTGAAGAGATGATGATGATGATGATGATGATGATG 358
 DB 307 ACAAGAGTACGGCATCAACCGTGAAGAGATGATGATGATGATGATGATGATGATG 364

RESULT 15
 US-10-739-930-5298
 ; Sequence 5298, Application US/10739930
 ; Publication No. US20040216190A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
 ; FILE REFERENCE: 38-21(53377)B
 ; CURRENT APPLICATION NUMBER: US/10/739,930
 ; CURRENT FILING DATE: 2003-12-18
 ; NUMBER OF SEQ ID NOS: 11088
 ; SEQ ID NO 5298
 ; LENGTH: 2869
 ; TYPE: DNA
 ; ORGANISM: Triticum aestivum
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER730_1608
 US-10-739-930-5298

Query Match 64.0%; Score 246.4; DB 18; Length 2869;
 Best Local Similarity 80.3%; Pred. No. 1.3e-65;
 Matches 289; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1 CAACGGGACCAAGCTTGATCATTTGGGTCGACCGGCTCCGAGCTGAGATCGCG 60
 DB 1988 GACCCGACCAACAGCTGATCATCATATATGACATCTGTTCTGAGTAGAGATTGCTG 2047
 QY 61 GCAATGCGGCGGACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 DB 2048 TGAAGGCTGCGGAG 2107
 QY 121 CTTGGGAATCTTTTGTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 180

DB 2108 GCTGGGAATCTTTGACAGAGCATGATGATGATGATGATGATGATGATGATGATG 2167
 QY 181 TCACAGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 DB 2168 TCACGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2227
 QY 241 CCCAAGGCAAGGCTTGGCATGCAAGTTCGGCGGAGTCTCTGCGGAGAGATCT 300
 DB 2228 CCAAGGCAAGGCTTGGCATGCAAGTTCGGCGGAGTCTCTGCGGAGAGATCT 2287
 QY 301 ACAAGAGTACGGCATCAACCGTGAAGAGATGATGATGATGATGATGATGATGATG 360
 DB 2288 ACAAGAGTACGGCATCAACCGTGAAGAGATGATGATGATGATGATGATGATGATG 2347

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 Job time : 437.803 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-300-482-569

Perfect score: 264
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 5: /cgn2_6/prodata/1/ina/6CTUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51.2	19.4	7218	1	US-08-232-463-14 Sequence 14, Appl
2	36.6	13.9	148794	4	US-09-949-016-12751 Sequence 12751, A
3	34.8	13.2	107820	4	US-09-792-616-1 Sequence 1, Appl
4	34.2	13.0	197336	4	US-09-949-016-12881 Sequence 12881, A
5	34.2	13.0	197337	4	US-09-949-016-14376 Sequence 14376, A
6	34.2	13.0	234288	4	US-09-949-016-17272 Sequence 17272, A
7	33	12.5	4412	4	US-09-949-016-14044 Sequence 14044, A
8	32.8	12.4	69263	4	US-09-949-016-12594 Sequence 12594, A
9	32.8	12.4	69709	4	US-09-949-016-16036 Sequence 16036, A
10	32.8	12.4	122772	4	US-09-949-016-14132 Sequence 14132, A
11	32.6	12.3	106380	4	US-09-949-016-17553 Sequence 17553, A
12	32.4	12.3	857	4	US-09-509-7128-31 Sequence 31, Appl
13	32	12.1	4082	4	US-09-949-016-22722 Sequence 22722, Ap
14	32	12.1	14205	4	US-09-949-016-14664 Sequence 14664, A
15	31.4	11.9	279	4	US-09-248-796A-7005 Sequence 7005, Ap
16	31.4	11.9	800	4	US-09-765-298A-17 Sequence 17, Appl
17	31.4	11.9	4002	3	US-09-356-952-9 Sequence 9, Appl
18	31.4	11.9	5415	4	US-09-976-594-311 Sequence 311, App
19	31.2	11.8	53526	3	US-08-658-136-2 Sequence 2, Appl
20	31.2	11.8	53577	3	US-08-658-136-1 Sequence 1, Appl
21	31	11.7	17879	4	US-09-949-016-12992 Sequence 12992, A
22	31	11.7	18474	4	US-09-949-016-17559 Sequence 17559, A
23	31	11.7	56963	4	US-09-949-016-12966 Sequence 12966, A
24	31	11.7	56968	4	US-09-949-016-11888 Sequence 11888, A
25	31	11.7	187136	4	US-09-949-016-17231 Sequence 17231, A
26	30.8	11.7	141560	4	US-09-949-016-16476 Sequence 16476, A
27	30.6	11.6	289	3	US-09-007-005-17 Sequence 17, Appl

C 28	30.6	11.6	289	3	US-09-244-796-17	Sequence 17, Appl
C 29	30.6	11.6	57726	4	US-09-949-016-16430	Sequence 16430, A
C 30	30.6	11.6	221545	4	US-09-949-016-13875	Sequence 13875, A
C 31	30.4	11.5	304533	4	US-09-949-016-15371	Sequence 15371, A
C 32	30.4	11.5	304533	4	US-09-949-016-15372	Sequence 15372, A
C 33	30.4	11.5	390416	4	US-09-949-016-16923	Sequence 16923, A
C 34	30.2	11.4	601	4	US-09-949-016-201472	Sequence 201472, A
C 35	30.2	11.4	601	4	US-09-949-016-201473	Sequence 201473, A
C 36	30.2	11.4	58782	4	US-09-949-016-16851	Sequence 16851, A
C 37	30.2	11.4	86639	4	US-09-949-016-17397	Sequence 17397, A
C 38	30	11.4	690	4	US-09-248-796A-1546	Sequence 1546, Ap
C 39	30	11.4	16924	4	US-09-949-016-13720	Sequence 13720, A
C 40	30	11.4	100877	4	US-09-949-016-13276	Sequence 13276, A
C 41	30	11.4	294836	3	US-09-949-016-15974	Sequence 15974, A
C 42	29.8	11.3	1798	3	US-08-687-691B-1	Sequence 1, Appl
C 43	29.8	11.3	9409	4	US-09-949-016-17121	Sequence 17121, A
C 44	29.8	11.3	12222	4	US-09-949-016-12238	Sequence 12238, A
C 45	29.8	11.3	12223	4	US-09-949-016-14119	Sequence 14119, A

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHRIFFINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304772/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 883-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZ9PT-F15
US-08-232-463-14
Query Match 19.4%; Score 51.2; DB 1; Length 7218;


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RESULT 5
US-09-949-016-14376
: Sequence 14376, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: FILE REFERENCE: CU001307
: CURRENT APPLICATION NUMBER: US/09/949, 016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14376
: LENGTH: 197337
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(197337)
: OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14376

Query Match      13.0%; Score 34.2; DB 4; Length 197337;
Best Local Similarity 52.4%; Pred. No. 1.7;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY      73  AAGCGCTTGGCCCGGAGATTCTCGTCTCAGCCTTCAACCTTTCATCGCTTTA 132
Db      14519 AGTGCCAGGCGCCCTGGAGAGCTTCGTGCTCTCTCTCTCCCTTCCCTCCCTCCCTC 14578

QY      133  ATCAAAACTTAACTATCCGCTCCCTCCGATTCATTCAGTCGCTCCCTTAAACCT 192
Db      14579 CTCCTGCACTCTCTCCCTCCCTCCCTCCCTCCGATCCCTCCCTCCCTCCCTCC 14638

QY      193  CCTTAGGATCAATGCTCCCA 215
Db      14639 CCTCTGACAGATGGCTGGCCA 14661

RESULT 6
US-09-949-016-17272
: Sequence 17272, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: FILE REFERENCE: CU001307
: CURRENT APPLICATION NUMBER: US/09/949, 016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 17272
: LENGTH: 234288
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: misc_feature

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; LOCATION:(1)...(234289)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17272

Query Match      13.0%; Score 34.2; DB 4; Length 234288;
Best Local Similarity 52.4%; Pred.No.1.8;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

OY 73 AAGCGCTTGGCCCCGAGATTCTGGCTTCCTCACCCTTAACCTTTCCATCGCTTTA 132
Db 14519 AGTGCCCAAGGCCCTGGAGAGGCTCTGGCTTCCTTCCTTCCTTCCTCCCTCCCTTC 14578

OY 133 ATCAAAACAATCAACTATCCGCTTCCTCCCGCATCATTCACGTGCCTCCTTAACCT 192
Db 14579 CTCCTGACATCTCCCTCCCTTCCTTCCTCCATCCCTTCCTCCCTCCCTGCTCC 14638

OY 193 CCTTAGCATCAAAATGCTCCCA 215
Db 14639 CTTCTGTGACGATGCTGCCA 14661


RESULT 7
US-09-949-016-14044/c
Sequence 14044, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14044
LENGTH: 4412
TYPE: DNA
ORGANISM: Human
US-09-949-016-14044

Query Match      12.5%; Score 33; DB 4; Length 4412;
Best Local Similarity 54.5%; Pred.No.0.59;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

OY 78 CTGCGCCCCGAGATTCGTGGCTTCACTTCAAACCTTCCTTCATGCGCTTTATAC 137
Db 335 CTCCTCCCTCTCTCTCTTCTCTCTCCCTTCCTTCCTCATCTCCCTCTCTTCTCTTC 276

OY 138 AAAATACTATTCGCGCTTCCTCCGATCATCATCACTGCTCCCTTTAAAACCTCTTA 197
Db 275 CTCCTCTCTCTCTCTCTCTCTCTCCCTCCCTTCCTTTCTCTCCCTTCCTTCCTTC 216

OY 198 C 198
Db 215 C 215


RESULT 8
US-09-949-016-12594/C
Sequence 12594, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016

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;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 12594
;; LENGTH: 69263
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)---(69263)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12594

Query Match 12.4%; Score 32.8; DB 4; Length 69263;
Best Local Similarity 54.0%; Pred. No. 3;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 115 CTTCTTCATCGCTTTTATACAAACTAACCTATCCGCTTCCGATCCATTCACT 174
DB 59885 CTGCTTCAGTGTATATAACATTAAGAGAACCAACCGTTAATTACCAAT 59826
QY 175 CGCTCCCTTTAAACCTCTTACGATCAATGCTCCCAACAGATGGAATGCAAGTC 234
DB 59825 CTCTACTCCCTTAATCTTTCTCAGAGATTAATTAAACAATTTCTTGATAGTATGTT 59766
QY 235 CTGC 238
DB 59765 CTTC 59762

RESULT 9
US-09-949-016-16036/c
; Sequence 16036, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16036
; LENGTH: 69709
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)---(69709)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16036

Query Match 12.4%; Score 32.8; DB 4; Length 69709;
Best Local Similarity 54.0%; Pred. No. 3;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 115 CTTCTTCATCGCTTTTATACAAACTAACCTATCCGCTTCCGATCCATTCACT 174
DB 59885 CTGCTTCAGTGTATATAACATTAAGAGAACCAACCGTTAATTACCAAT 59826

QY 175 CGCTCCCTTTAAACCTCTTACGATCAATGCTCCCAACAGATGGAATGCAAGTC 234
DB 59825 CTCTACTCCCTTAATCTTTCTCAGAGATTAATTAAACAATTTCTTGATAGTATGTT 59766
QY 235 CTGC 238
DB 59765 CTTC 59762

RESULT 10
US-09-949-016-14132/c
; Sequence 14132, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14132
; LENGTH: 122772
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14132

Query Match 12.4%; Score 32.8; DB 4; Length 122772;
Best Local Similarity 59.8%; Pred. No. 4.1;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 16 TCCCAATGCGCTTCGTTTCCAGCTTCAAGCCCAATTCAGTGTATACAGAG 75
DB 78404 TCACAAATGCGCTTGAATTTGACACCCAGAACCCCAATTCAGTGTATGCTGCTCAT 78345
QY 76 CGTTGCGCCCGGAGATTTCGTTCTCACC 107
DB 78344 GGCACCCCTCAATATCTTAATCTTCTCACC 78313

RESULT 11
US-09-949-016-17553/c
; Sequence 17553, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17553
; LENGTH: 106380
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17553

Query Match 12.3%; Score 32.6; DB 4; Length 106380;

Best Local Similarity 58.9%; Pred. No. 4.5;
Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 137 CAAACTACCTATCCGCTCCCTCCGATTCATTCAGTCCCTCTTAAACCTCCTT 196
DB 28232 CAAACCTAACCACTATCTAGTATCTTCCATTCCTTCATACGCTCTTCCCTCCCTC 28173

QY 197 ACGATCAATGCTTCCCAACAGATGGGAATGGA 231
DB 28172 ATGATCTGATGCTCCTCAATATGCTGTGCA 28138

RESULT 12
US-09-509-712B-31/c

; Sequence 31, Application US/09509712B
; Patent No. 6777177

; GENERAL INFORMATION:

; APPLICANT: Rubin, Donald H.

; APPLICANT: Organ, Edward L.

; TITLE OF INVENTION: Mammalian Genes Involved in Viral

; FILE REFERENCE: 01123.0004

; CURRENT APPLICATION NUMBER: US/09/509,712B

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: PCT/US98/21276

; PRIOR FILING DATE: 1998-10-08

; PRIOR APPLICATION NUMBER: 60/062,021

; PRIOR FILING DATE: 1997-10-10

; NUMBER OF SEQ ID NOS: 127

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 31

; LENGTH: 857

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: 1- 857

; OTHER INFORMATION: n = g, a, c or t (u)

US-09-509-712B-31
Query Match 12.3%; Score 32.4; DB 4; Length 857;
Best Local Similarity 47.5%; Pred. No. 0.41;
Matches 66; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 62 TTCCTATCAGAAAGGCTTGGCCCCGAGATTCTCGCTTCTCCTTCAAACTTCTTC 121
DB 248 TTGCAGATNAGAACCTCANTCTTTCGANGTCTGTGTTCCCAACCCNTACANCGTCTNC 189

QY 122 CATCGCTTTTATATCAAAACTAACCTTATCGGCTTCCCTCGATCCATTCTGCTGCC 181
DB 188 TTTTCCGTTTGGCAGCATCCCAACNTTCCCTANTCCGCCGACCGTTCTGTTGTC 129

QY 182 TCTTAAACCTCTTACCG 200
DB 128 NCCGTGAAATTTTTCG 110

RESULT 13

US-09-949-016-2722
; Sequence 2722, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2722

; LENGTH: 4082

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-2722

Query Match 12.1%; Score 32; DB 4; Length 4082;
Best Local Similarity 50.7%; Pred. No. 1.3;
Matches 77; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 26 TTCGTTTCCAGCTCTTACAGCCAAATCCACTTCTCTTATACAGAGCGCTTGGCC 85
DB 118 TCCGGGTCCTCCCTGCGCCACCTTATCCACTCTCTCTTCCGATTCCTCTGCTC 177

QY 86 CCGAATTCGCTTCCCTCCACCTTCAACCTTCTTCCATCGCTTTATACAAACTAA 145
DB 178 ACCCATCTCTCTCCGCGCCCTTCTGATTCCTCACCCTCTGATTCCTCTCGC 237

QY 146 CCTATCCGCTTCCCTCCGATCCATTCACTCGC 177
DB 238 CTTTCCAGAGACCCAGAGCCCTGACCC 269

RESULT 14
US-09-949-016-14464

; Sequence 14464, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14464

; LENGTH: 14205

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14464

Query Match 12.1%; Score 32; DB 4; Length 14205;
Best Local Similarity 50.7%; Pred. No. 2.5;
Matches 77; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 26 TTCGTTTCCAGCTCTTACAGCCAAATCCACTTCTCTTATACAGAGCGCTTGGCC 85
DB 2118 TCCGGGTCCTCCCTGCGCCACCTTATCCACTCTCTCTTCCGATTCCTCTGCTC 2177

QY 86 CCGAATTCGCTTCCCTCCACCTTCAACCTTCTTCCATCGCTTTATACAAACTAA 145
DB 2178 ACCCATCTCTCTCCGCGCCCTTCTGATTCCTCACCCTCTGATTCCTCTCGC 2237

QY 146 CCTATCCGCTTCCCTCCGATCCATTCACTCGC 177
DB 2238 CTTTCCAGAGACCCAGAGCCCTGACCC 2269

RESULT 15

US-09-248-796A-7005/c

; Sequence 7005, Application US/09248796A

; Patent No. 6747137

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; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 7005
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-7005

Query Match      11.9%; Score 31.4; DB 4; Length 279;
Best Local Similarity 48.6%; Pred. No. 0.51;
Matches 86; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY      22  TGGCTTCGCTTCCAGACTCTCAAGGCCAATCCACTGCTTCCTTATCAGAAGCGCTTC 81
      Db      204  TCGATTCCTCTCTCTCTCTTGGCCCTTTTCTTCTCTCTCCGTCGCCCTCCT 145
QY      82  GCGCCCGAGATTCTGCGCTTCCACCTTCAACCTTCTTCATCGCTTTTATCACAAAA 141
      Db      144  TTCTTCTCTCTTCTTCTCTCTCTCTCCAGTTCCCCCCTTTTCCCCCTCCCTCTTC 85
QY      142  CTAACTATCCGCTTCCCTCCGATCCATTCACTGCTCCCTCTTAAACCTTCCTTAC 198
      Db      84  CTCTCTCTACTTTTCCCTCTTTTCAAGCTCTCTCTTGTGTCCTCCCTCCCTTTC 28

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 299.522 Seconds
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Title: US-09-300-482-569

Perfect score: 264
Sequence: 1 ctgactgcagcaatccca.....gacatgctcatgacttta 264

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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19: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	252	95.5	747	17	US-10-424-599-43249
2	215.8	81.7	1926	17	US-10-424-599-43247
3	196.8	74.5	592	17	US-10-424-599-43245
4	145	54.9	676	17	US-10-424-599-43250
5	100.6	38.1	346	17	US-10-424-599-10015
6	100.4	38.0	305	17	US-10-424-599-65148
7	96.8	36.7	322	17	US-10-424-599-33477
8	95	36.0	376	17	US-10-424-599-132643
9	83.6	31.7	169	17	US-10-424-599-41040
10	60.4	22.9	205	17	US-10-424-599-86542
11	58.2	22.0	289	17	US-10-424-599-28474

12	52.8	20.0	208	17	US-10-424-599-58838	Sequence 58838, A
13	47.6	18.0	603	18	US-10-021-323-1453	Sequence 1453, Ap
14	45.6	17.3	183	17	US-10-424-599-15721	Sequence 15721, A
15	44.2	16.7	320	17	US-10-424-599-102259	Sequence 102259, A
16	35.2	13.3	366	18	US-10-674-124A-15571	Sequence 15571, A
17	35.2	13.3	2000	9	US-09-938-842A-3388	Sequence 3388, Ap
18	35.2	13.3	2000	11	US-09-938-842A-3388	Sequence 3388, Ap
19	34.8	13.2	7329	17	US-10-221-714A-396	Sequence 396, App
20	34.8	13.2	57181	19	US-10-741-600-17781	Sequence 17781, A
21	34.8	13.2	107820	10	US-09-792-616-1	Sequence 1, Appl1
22	34.8	13.2	107820	18	US-10-764-328-1	Sequence 1, Appl1
23	34.8	13.2	172984	19	US-10-484-577-661	Sequence 661, Appl1
24	34.6	13.1	3673778	16	US-10-312-841-2	Sequence 2, Appl1
25	34.4	13.0	2672	9	US-09-775-938A-34	Sequence 34, Appl1
26	34.2	13.0	263852	18	US-10-812-232-6	Sequence 6, Appl1
27	34.2	13.0	276820	17	US-10-271-416-9	Sequence 9, Appl1
28	34	12.9	31724	13	US-10-087-192-766	Sequence 766, App
29	34	12.9	53222	18	US-10-331-053-76	Sequence 76, Appl1
30	33.6	12.7	341	18	US-10-674-124A-12122	Sequence 12122, A
31	33.4	12.7	630	17	US-10-388-934-181	Sequence 381, App
32	33.2	12.6	5647	15	US-10-311-455-1540	Sequence 1540, Ap
33	33.2	12.6	6547	17	US-10-221-613-282	Sequence 282, App
34	33.2	12.6	6531	15	US-10-311-455-613	Sequence 613, App
35	33	12.5	9007	17	US-10-221-714A-337	Sequence 337, App
36	32.8	12.4	308	17	US-10-424-599-9496	Sequence 9496, Ap
37	32.8	12.4	468	17	US-10-424-599-79082	Sequence 79082, A
38	32.8	12.4	969	18	US-10-363-345A-1397	Sequence 1397, Ap
39	32.8	12.4	969	18	US-10-363-345A-1398	Sequence 1398, Ap
40	32.8	12.4	969	19	US-10-363-483A-1397	Sequence 1397, Ap
41	32.8	12.4	969	19	US-10-363-483A-1398	Sequence 1398, Ap
42	32.6	12.3	650	13	US-10-027-632-216903	Sequence 216903, A
43	32.6	12.3	650	17	US-10-027-632-216903	Sequence 216903, A
44	32.6	12.3	2074	17	US-10-425-114-6140	Sequence 6140, Ap
45	32.6	12.3	2327	17	US-10-424-599-121972	Sequence 121972, A

ALIGNMENTS

RESULT 1
US-10-424-599-43249
Sequence 43249, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 43249
LENGTH: 747
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(747)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_139052C.1
US-10-424-599-43249

Query Match 95.5%; Score 252; DB 17; Length 747;
Best Local Similarity 99.6%; Pred. No. 4.8e-72;
Matches 263; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Db 116 TCACCTGCAGCAATCCCAATGCTTCCTTCACAGCTTCACGCCAATCCTTC 175
OY 2 TCACCTGCAGCAATCCCAATGCTTCCTTCACAGCTTCACGCCAATCCTTC 61

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QY      62  TTCCTTATCAGAGCGCTTGGCCCCCGAGATTCTGCTTCTTCACTTCAAACTTCTTC 121
      176  TTCCTTATCAGAGCGCTTGGCCCCCGAGATTCTGCTTCTTCACTTCAAACTTCTTC 235
QY      122  CATGCGTTTAAATCAAAAATACTAATCGCTTCCCTCGATCCATTCACTGCTGCC 181
      236  CATGCGTTTAAATCAAAAATACTAATCGCTTCCCTCGATCCATTCACTGCTGCC 295
QY      182  TCTTAAAACTCCCTTACGAGTCAAAATGCTCCAAAACAGATGGAAATGGAAGTCTGCAA 241
      296  TCTTAAAACTCCCTTACGAGTCAAAATGCTCCAAAACAGATGGAAATGGAAGTCTGCAA 355
Db      242  GAGGACA-TGCTTCATGATCTTTA 264
QY      356  GAGGACAGTGTCTTCAATCTTTA 379
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RESULT 2
US-10-424-599-43247
; Sequence 43247, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 43247
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139050C.1
US-10-424-599-43247
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Query Match      81.7%; Score 215.8; DB 17; Length 1926;
Best Local Similarity 92.9%; Pred. No. 4,9e-60;
Matches 237; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY      11  GCAATTCGAATGCGTTCGTTCCAGCTCTCAAGCCAAATCCACTTGCCTTATC 70
      81  GCAATTCGAATGCGTTCGTTCCAGCTCTCAAGCTCTCAAGCTCTTCTTATC 140
QY      71  AGAAGCGCTTGGCCCCCGAGATTCTGCTTCTTCAAACTTCTTCATGCTTT 130
      141  AGAAGCGCTTGGCCCCCGAGATTCTGCTTCTTCAATCTTCTTCAAGCTAT 200
Db      131  TAATACAAAATACTATCGCTTCCCTCGATCCATTCACTGCTCCCTTTAAAC 190
      201  TAATACAAAATACTATCGCTTCCCTCGATCCATTCACTGCTCCCTTTAAAC 260
QY      191  CTCCTTAGGATCAAAATGCTCCAAAACAGATGGAAATGGAAGTCTGCAAGAGACA-T 249
      261  CTCCTTAGGATCAAAATGCTCCAAAACAGATGGAAATGGAAGTCTGCAAGAGAGAGT 320
Db      250  GCTTCATGATCTTTA 264
QY      321  GCTTCATGATCTTTA 335
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RESULT 3
US-10-424-599-43245
; Sequence 43245, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
```

```
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 43245
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(592)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139049C.1
US-10-424-599-43245
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Query Match      74.5%; Score 196.8; DB 17; Length 592;
Best Local Similarity 88.8%; Pred. No. 5.4e-54;
Matches 213; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY      2  TGACTTGAGCAATTCGAATGCTTCCGTTTCCAGCTCTCAAGCCAAATCCACTTGC 61
      10  TGACTTGAGCAATTCGAATGCTTCCGTTTCCAGCTCTCAAGCTCTCAAGCTTGC 69
QY      62  TTCCTTATCAGAGCGCTTGGCCCCCGAGATTCTGCTTCTTCACTTCAAACTTCTTC 121
      70  TTCCTTATCAGAGCGCTTGGCCCCCGAGATTCTGCTTCTTCACTTCAAACTTCTTC 129
QY      122  CATGCGTTTAAATCAAAAATACTAATCGCTTCCCTCGATCCATTCACTGCTGCC 181
      130  CATGCGTTTAAATCAAAAATACTAATCGCTTCCCTCGATCCATTCACTGCTGCC 189
Db      182  TCTTAAAACTCCCTTACGAGTCAAAATGCTCCAAAACAGATGGAAATGGAAGTCTGCAA 241
      190  TCTTAAAACTCCCTTACGAGTCAAAATGCTCCAAAACAGATGGAAATGGAAGTCTGCAA 249
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RESULT 4
US-10-424-599-43250
; Sequence 43250, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 43250
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(676)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139053C.1
US-10-424-599-43250
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Query Match      54.9%; Score 145; DB 17; Length 676;
Best Local Similarity 91.1%; Pred. No. 5.4e-37;
Matches 154; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      31  TTCGAAGCTCTCAAGCCAAATCCACTTGTCTTATCAAGAGCGCTTGGCCCCGAG 90
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Db 4 TTTTCAAGCTCCAGAGGCATCTCCAGCGCTTCCTTATCAGAGGCTTCGCCAGAG 63
QY 91 ATTTCGCTCTCTCACTTCAAACTTCTTCATCGCTTTTATCAAACTAATCTAT 150
Db 64 ATTTCGCTCTCTCTCACTTCAAACTTCTTCATCGCTTTTATCAAACTAATCTAT 123
QY 151 CGGCTTCCCTCGATCCATTCATCGCTCTCTTAAACCTTCCTAG 199
Db 124 CCGCTTCCCTCGATCCATTCATCGCTCTCTTAAACCTTCCTAG 172

RESULT 5
US-10-424-599-10015
; Sequence 10015, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 10015
; LENGTH: 346
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_109053C.1
US-10-424-599-10015

Query Match 38.1%; Score 100.6; DB 17; Length 346;
Best Local Similarity 68.5%; Pred. No. 1.5e-22;
Matches 139; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
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Db 3 CTCCTACCAATGTCTCTCACTTACCAAAACCGCTACGCTCAAAATTCAAATTCCT 62
QY 106 CTTTCAACCTTCTCTCTCTTATCAAGAACTAATCTATCTCTCTCTCAT 165
Db 63 GGGCAATTCCT 122
QY 166 CCATTCACCT 225
Db 123 TCATACACTGGCT 182
QY 226 ATGAAGTCT 248
Db 183 ATGTAAGTCT 205

RESULT 6
US-10-424-599-69148
; Sequence 69148, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 69148
; LENGTH: 305

; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(305)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13453C.1
US-10-424-599-69148

Query Match 38.0%; Score 100.4; DB 17; Length 305;
Best Local Similarity 72.3%; Pred. No. 1.7e-22;
Matches 107; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 2 TCACCTTGACGCAATTCCTTCCAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 61
Db 158 TNNNTNACGCTATTCNNANTGNNNTCTNNNTNNNNNNNNNNNNNNNNNNNN 217
QY 62 TTCCTTATCAGAAAGGCTTCCGCCGAGATTCCTCTCTCTCTCTCTCTCTCTCT 121
Db 218 TNCCTGATCAGAGGCTGNGCCGAGANTTNTGTCTCTCTCTCTCTCTCTCTCT 277
QY 122 CATCGCTTTTATCAAACTAATCTA 149
Db 278 CATCGCTTTTATCACTAATCTA 305

RESULT 7
US-10-424-599-33477
; Sequence 33477, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 33477
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130233C.1
US-10-424-599-33477

Query Match 36.7%; Score 96.8; DB 17; Length 322;
Best Local Similarity 84.0%; Pred. No. 2.6e-21;
Matches 121; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 122 CATCGCTTTTATCAAACTAATCTAATCTCTCTCTCTCTCTCTCTCTCTCTCT 181
Db 1 CAACACTATTAATTCAGAAATTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
QY 182 TCTTAAACCT 241
Db 61 TCTTAAACCT 120
QY 242 GAGGAC-ATGCTTCATGATCTTTA 264
Db 121 CAGGACAACTACTTCAATGATCTTTA 144

RESULT 8
US-10-424-599-132643
; Sequence 132643, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 132643
LENGTH: 376
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_90784C.1
US-10-424-599-132643

Query Match 36.0%; Score 95; DB 17; Length 376;
Best Local Similarity 67.6%; Pred. No. 1.1e-20;
Matches 148; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

QY 2. ATGGCTTCGCTTCCAGCTCTCAAGCCCAATCCACTTCTTATCAGAGCGCTT 80
DB : ATGGCTTCATTTTCAGCTCTCAAGCCCAATCCACTTCTTATCAGAGCGCTT 60
QY 81. CGCCCCGAGATTCGCTTCTCACCCTTCAAACTTCTTCATGCTTTTATCAGAA 140
DB 61. CCGAAAAAGAAAAAG-GACACCATATCCCTCCATATGACCAAGTGTGAAGTACCA 119
QY 141. ACTAACCTATCGCTTCCCTCCGATCCATTCAGTGCCTCCCTTAAACCTCTTACCG 200
DB 120. ACGGACTATTCGATTCCTCCATGACCATTCACCTCCCTCGTGTATCTGCAATGAG 179
QY 201. ATCAATGCTCCCAACAGATGGAGATGGAAGTCCGCA 239
DB 180. AACAAATGCTCCGTCACATTTGACGACGATGACTTACA 218

RESULT 9

US-10-424-599-41040
Sequence 41040, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 41040
LENGTH: 169
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_13705C.1
US-10-424-599-41040

Query Match 31.7%; Score 83.6; DB 17; Length 169;
Best Local Similarity 87.7%; Pred. No. 4.4e-17;
Matches 114; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 136. ACAAACCTAATCCGCTTCCCTCCGATCCATTCAGTGCCTCCCTTAAACCTCCT 195
DB 9. ACAAAAGGAACCTCCGCTTCCCTCCGATCCATTCAGTGCCTCCCTTAAACCTCCT 68
QY 196. TAC-GAGTCAATCTCCCAACAGATGGAGATGGAAGTCTGCAAGAGAGACA-TGCTT 253
DB 69. TCGGGGCTCAATCTCCCAATCAGATGGAGATGGAAGTCTGCAAGAGAGACAGTCTT 128

QY 254. CATGATCTTT 263
DB 129. CAGGCTCTTT 138

RESULT 10
US-10-424-599-86542
Sequence 86542, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 86542
LENGTH: 205
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_49159C.1
US-10-424-599-86542

Query Match 22.9%; Score 60.4; DB 17; Length 205;
Best Local Similarity 91.5%; Pred. No. 1.9e-09;
Matches 75; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 182. TCTTAAACCTCTTACGATCAATGCTCCCAACAGATGGAGATGGAAGTCTGCAAA 241
DB 1. TCTTAAACCTCTTACGATCAATGCTCCCAACAGATGGAGATGGAAGTCTGCAAA 60
QY 242. GAGGACA-TGCTTCATGATCTT 262
DB 61. GAGGACGCGCTTCATGATCTT 82

RESULT 11

US-10-424-599-28474
Sequence 28474, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 28474
LENGTH: 289
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_125713C.1
US-10-424-599-28474

Query Match 22.0%; Score 58.2; DB 17; Length 289;
Best Local Similarity 89.2%; Pred. No. 1.1e-08;
Matches 74; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 182. TCTTAAACCTCTTACGATCAATGCTCCCAACAGATGGAGATGGAAGTCTGCAAA 241
DB 1. TCTTAAACCTTATTCGATCAATGCTCCCAACAGATGGAGATGGAAGTCTGCAAA 60
QY 242. GAGGACA-TGCTTCATGATCTT 263

Db 61 GAGACAGAGCTTCATGATCTAT 83

RESULT 12

US-10-424-599-58838

Sequence 58838, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 58838

LENGTH: 208

TYPE: DNA

ORGANISM: Glycine max

FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_24142C.1

US-10-424-599-58838

Query Match 20.0%; Score 52.8; DB 17; Length 208;

Best Local Similarity 84.5%; Pred. No. 5.9e-07;

Matches 71; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Db 182 TCTTAAACCTCTTACGATCAATGCTCCCAAGATGGATGGAATGCTTCCGAA 241

1 TGTTAAGACCGGCTTACGATGAGCTCCGAGACAGGTGGAAATGAAATCTGCGACA 60

Qy 242 GAGGAC-ATGCTTCATGATCTTTA 264

Db 61 GAGGACATGCTTACATGAGCTTTA 84

RESULT 13

US-10-021-323-1453

Sequence 1453, Application US/10021323

Publication No. US20040123340A1

GENERAL INFORMATION:

APPLICANT: Deikman, Jill

APPLICANT: Feng, Paul C.C.

APPLICANT: Fincher, Karen L.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

FILE REFERENCE: 38-21(52274)B

CURRENT APPLICATION NUMBER: US/10/021,323

CURRENT FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: US 60/255, 619

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 17880

SEQ ID NO 1453

LENGTH: 603

TYPE: DNA

ORGANISM: Gossypium hirsutum

FEATURE:

NAME/KEY: unsure

LOCATION: (1) (603)

OTHER INFORMATION: unsure at all n locations

OTHER INFORMATION: Clone ID: LIB8825-003-Q1-K6-E10

US-10-021-323-1453

Query Match 18.0%; Score 47.6; DB 18; Length 603;

Best Local Similarity 53.3%; Pred. No. 4.4e-05;

Matches 129; Conservative 0; Mismatches 104; Indels 9; Gaps 1;

Db 44 TTCTCATGAGCTACCATTTCCAGCTCGTAAACCCCAACCCAGCTTCTCTTTCATTA 103

Qy 75 GCGTTCCGCCCCGAGATTCGCTTCTTCTACCTTCAA-----CCTTCTTCATC 125

Db 104 TCTTCAACACGAGATCTTCTTCATGCTTAAATGCTTGTGGTCTTCCAGGCTC 163

Qy 126 GCTTTTATCAAAAACCTATCCGTTCCCTCCGATTCATTCATCGCTCCCTCTT 185

Db 164 GCTTCAGCTTACAGCTGTTTCATCTTCTAGCTTGTCTCGATTAACCAACCTTTC 223

Qy 186 AAACCTCCTTACGATCAATGCTCCCAACAGATGGATGAATGAAATGCTTCCAAAGAG 245

Db 224 AGGGGCTCTTGTGTGTCTGATGTTCTTCTGTGATGAAAGATGATGATGAAGAG 283

Qy 246 AC 247

Db 284 AC 285

RESULT 14

US-10-424-599-15721

Sequence 15721, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 15721

LENGTH: 183

TYPE: DNA

ORGANISM: Glycine max

FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_114200C.1

US-10-424-599-15721

Query Match 17.3%; Score 45.6; DB 17; Length 183;

Best Local Similarity 73.3%; Pred. No. 0.00013;

Matches 85; Conservative 0; Mismatches 29; Indels 2; Gaps 2;

Qy 151 CGGCTTCCCTCGATCCATTCAGTCCCTCTTAAACCTCCT-TACGATCAATGC 209

Db 8 CCGTGACCTCGATTCATTCCTATATCCAGTTAAACCTCTCTACGTGCGATAGGC 67

Qy 210 TCCCAACAGATGGAATGGAAGTCCCTGMAAGAGACAT-GCTTCATGATCTTTA 264

Db 68 CTCCTATATATGCGAGTGAGAGCCCTGCCAGAGAGCGTGCCTCATATCTTTA 123

RESULT 15

US-10-424-599-102259

Sequence 102259, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 102259

LENGTH: 320

TYPE: DNA

ORGANISM: Glycine max

FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_114200C.1

US-10-424-599-102259

Query Match 17.3%; Score 45.6; DB 17; Length 183;

Best Local Similarity 73.3%; Pred. No. 0.00013;

Matches 85; Conservative 0; Mismatches 29; Indels 2; Gaps 2;

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; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63357C.1
US-10-424-599-102259

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Query Match      16.7%; Score 44.2; DB 17; Length 320;
Best Local Similarity 75.3%; Pred. No. 0.00045;
Matches 55; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY      176 GCTCCCTTTAAACCTCTTACGATCAATGCTCCCAACACAGATGGAGATGGAAGTCC 235
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db       1 GCTACACGTTCAATCTTAATATGTTCAATGCTTCCAACACAGATGGAGATGGAAGTCC 235

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QY      236 TGCACAGAGGACA 248
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db       61 TGTATAGCTGACA 73

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Search completed: May 4, 2005, 21:11:51
Job time : 303.522 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:02:12 / Search time 87.7858 Seconds
(without alignments)
5591.830 Million cell updates/sec

Title: US-09-300-482-619

Perfect score: 300
Sequence: 1 gattctatgcacacacccgat.....ttcagaatgtctgtctgrrg 300

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6C_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/6D_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	30.3	269	4	US-09-313-294A-2271
2	74	24.7	1590	4	US-09-902-540-5815
3	74	24.7	72704	4	US-09-902-540-1273
4	33.6	11.2	1200	4	US-09-134-000C-2307
5	33.2	11.1	601	4	US-09-949-016-163223
6	33.2	11.1	80004	4	US-09-949-016-16318
7	33	11.0	78630	4	US-09-949-016-16790
8	33	11.0	197336	4	US-09-949-016-12881
9	33	11.0	197337	4	US-09-949-016-14376
10	33	11.0	234288	4	US-09-949-016-17272
11	32.6	10.9	601	4	US-09-949-016-176915
12	32.6	10.9	300598	4	US-09-949-016-11868
13	32.6	10.9	302604	4	US-09-949-016-14588
14	32.6	10.9	302604	4	US-09-949-016-14589
15	32.6	10.9	308362	4	US-09-949-016-17119
16	32.4	10.8	543	4	US-08-956-171E-931
17	32.4	10.8	543	4	US-08-781-986A-931
18	32.4	10.8	265038	4	US-09-949-016-15779
19	32.2	10.7	601	4	US-09-949-016-200076
20	32.2	10.7	832	4	US-09-621-976-2813
21	31.6	10.5	1437	4	US-09-134-000C-2814
22	31.4	10.5	2034	4	US-09-543-681A-3764
23	31.4	10.5	13977	3	US-09-484-970B-60
24	31	10.3	601	4	US-09-949-016-200077
25	31	10.3	84296	4	US-09-949-016-17375
26	30.8	10.3	531	4	US-09-621-976-1177
27	30.8	10.3	579	3	US-09-026-017-1

28	30.8	10.3	579	3	US-09-631-547-1	Sequence 1, Appl
29	30.8	10.3	601	4	US-09-949-016-140812	Sequence 140812, A
30	30.8	10.3	264358	4	US-09-949-016-15725	Sequence 15725, A
31	30.6	10.2	1051	3	US-08-961-083-125	Sequence 125, Appl
32	30.6	10.2	1051	3	US-09-536-784-125	Sequence 125, Appl
33	30.6	10.2	13206	3	US-08-961-527-33	Sequence 164, Appl
34	30.6	10.2	22243	4	US-08-956-171E-164	Sequence 164, Appl
35	30.6	10.2	22243	4	US-08-781-986A-164	Sequence 63183, A
36	30.4	10.1	601	4	US-09-949-016-63183	Sequence 12348, A
37	30.4	10.1	38239	4	US-09-949-016-12348	Sequence 13570, A
38	30.2	10.1	38252	4	US-09-949-016-13570	Sequence 12461, A
39	30.2	10.1	93920	4	US-09-949-016-12461	Sequence 15390, A
40	30.2	10.1	93920	4	US-09-949-016-15390	Sequence 16274, A
41	30.2	10.1	235064	4	US-09-949-016-16274	Sequence 63182, A
42	30.2	10.1	238815	4	US-09-949-016-63182	Sequence 14009, A
43	30	10.0	601	4	US-09-949-016-14009	Sequence 17543, A
44	30	10.0	24841	4	US-09-949-016-17543	
45	30	10.0	36546	4	US-09-949-016-17543	

ALIGNMENTS

```

RESULT 1
US-09-313-294A-2271
Sequence 2271, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 2271
LENGTH: 269
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Inocyte ID No. 6476212 700552402H1
NAME/KEY: unsure
LOCATION: 199, 202, 205, 208, 230-231, 236, 240, 244, 248, 253, 256, 259, 267
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-2271
Query Match 30.3%; Score 91; DB 4; Length 269;
Best Local Similarity 88.2%; Pred. No. 7.1e-22;
Matches 105; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
Db 1 GATTATTGACAAACCGATCCTGCTGGATTGATCATCAATTCCTCACTAGGACCTG 60
124 GATTATTGACAAACCAATCTCTGCTGATTCATCAATTCCTCACTAGGACCTG 183
61 AACTGGCACTACTCTTGTATTTGTCATTTCATTAAGAGCGAGGACACCTGAACCCGC 119
164 AACTGGCACTACTCTTGTATTTGTCATTTCATTAAGAGCGAGGACACCTGAACCCGC 241
RESULT 2
US-09-902-540-5815
Sequence 5815, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B

```

;; CURRENT APPLICATION NUMBER: US/09/902,540
;; CURRENT FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: 60/217,883
;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 16825
;; SEQ ID NO 5815
;; LENGTH: 1590
;; TYPE: DNA
;; ORGANISM: Myxococcus xanthus
US-09-902-540-5815

Query Match 24.7%; Score 74; DB 4; Length 1590;
Best Local Similarity 53.0%; Pred. No. 1.9e-15;
Matches 158; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 3 TTATTTGACAAACCCGATCTCTGGATGATGATCAATTCCTCAACTAGACCTGAA 62
DB 439 TTCTTGACAAACCGACCGGACCGGCTGACCGCTGCGCAACTGGCGGACGG 498
QY 63 CTGGCACTACTCTGTTGATTTCTTAAGAGCGGACACCTGAAACCGGCAT 122
DB 499 CTGTCGAGAGCGCTCACCCCTGCTATCAGCAAGTGGGTGGCAAGAGAGCGGCAC 558
QY 123 GGTCTACTAGAACTACGAAAGCCTTCAGATCGGGGCTGCATTTCTGAAACAGGGT 182
DB 559 GGCATGCTGAGGCGCGGCGGCTACTCGGCGCGGCGCTGACTTCAGCAAGCAGCC 618
QY 183 GTTGCAATTAATCAAGAAATCTCTGTGGAGTAACCTGTAAGATAGAGGATGTTA 242
DB 619 GTGGCCGTACACCGGCGCGGACGAGCTGGACACACCGGAAAGAGAGGCTGGCTG 678
QY 243 GCTCGGTTTCTATGTTGATTGGTGTGTGATGAGACTTCAGAAATGCTGCTGTG 300
DB 679 CGGCGCTTCCCATGTGGGACTGTGGGTGGCGGCGGACGTGCTGACGTCCGCGGTG 736

RESULT 3
US-09-902-540-1273/c
Sequence 1273; Application US/0902540
GENERAL INFORMATION:
PATENT NO. 6833447
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1273
LENGTH: 72704
TYPE: DNA
ORGANISM: Myxococcus xanthus
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(72704)
OTHER INFORMATION: unsure at all n locations
US-09-902-540-1273

Query Match 24.7%; Score 74; DB 4; Length 72704;
Best Local Similarity 53.0%; Pred. No. 1.5e-14;
Matches 158; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 3 TTATTTGACAAACCCGATCTCTGGATGATGATCAATTCCTCAACTAGACCTGAA 62
DB 33865 TTCTTGACAAACCGACCGGACCGGCTTCAACCGGCTGGCGCAACTGGCGGACGG 33806
QY 63 CTGGCACTACTCTTGTATTTCTTAAGAGCGGACACCTGAAACCGGCAT 122
DB 33805 CTGTCGAGAGCGCTCACCCCTGCTATCAGCAAGTGGGTGGCAAGAGAGAGCGGCAC 33746

QY 123 GGTCTACTAGAAAGTACAGAAAGCCTTCAGAGATGGGGGCTCAATTCGAAACAGGT 182
DB 33745 GGCATCTGAGAGCCGAGCGCGGCTACTGCGCGCGGCTGACTGACGACAGCAGCC 33686
QY 183 GTTGCAATTAATCAAGAAATCTCTGTTGATTAACACTGCTAGAAATAGAGGATGTTA 242
DB 33685 GTGGCCGTACCGGCGCGGACGAGCTGACAAACACCGGAAAGAGAGGCTGGCTG 33626
QY 243 GCTCGGTTTCTATGTTGATTGGTGTGTGATGAGACTTCAGAAATGCTGCTGTG 300
DB 33625 CGGCGCTTCCCATGTGGGACTGTGGGTGGCGGCGGACGTGACGTCCGCGGTG 33568

RESULT 4
US-09-134-000C-2307/c
Sequence 2307; Application US/09134000C
PATENT NO. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucetle-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2307
LENGTH: 1200
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-2307

Query Match 11.2%; Score 33.6; DB 4; Length 1200;
Best Local Similarity 56.2%; Pred. No. 0.28;
Matches 63; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 126 CTACTAGAGTACGAAAGCCTTCAGAGATCGGGGCTGCAATTCGAAACAGGAGT 185
DB 301 CTAACACTAGTAATGCAATATTAAGACATAGAGATCGCATCGCCCAACAGGGGAA 242
QY 186 GCATTAATCTGAAAGAAATTCCTGTTGATTAACCTGCTGAATAGAGGAT 237
DB 241 TTTTCTCTCAAGGCGTTTCACCATGATTAAGCAATTAATAGATAAT 190

RESULT 5
US-09-949-016-163223/c
Sequence 163223; Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 163223
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-163223

Query Match 11.1%; Score 33.2; DB 4; Length 601;
Best Local Similarity 56.4%; Pred. No. 0.26;
Matches 62; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 112 AACCCGCAATGCTTACTAGAGTACAGAAAGCTTCAGAGATGCGGGCTGCATTCT 171
DB 580 AAGCCAGCAATGTGCAAAAAGCAAGAAAGCTGTATATAGATGAGTGCAGACTATA 521

QY 172 CGAAGCAGGTGTGCAATTAATTCATCAAGAAATTCCTGTGATTAACACT 221
DB 520 CGCAACGAGCTGTATTAATTTCTACAGCAATATCCACTGTATCAATTAATCTCT 471

RESULT 6
US-09-949-016-16318/C
Sequence 16318, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16318
LENGTH: 80004
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(80004)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16318

Query Match 11.1%; Score 33.2; DB 4; Length 80004;
Best Local Similarity 56.4%; Pred. No. 3.9;
Matches 62; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 112 AACCCGCAATGCTTACTAGAGTACAGAAAGCTTCAGAGATGCGGGCTGCATTCT 171
DB 13605 AAGCCAGCAATGTGCAAAAAGCAAGAAAGCTGTATATAGATGAGTGCAGACTATA 13546

QY 172 CGAAGCAGGTGTGCAATTAATTCATCAAGAAATTCCTGTGATTAACACT 221
DB 13545 CGCAACGAGCTGTATTAATTTCTACAGCAATATCCACTGTATCAATTAATCTCT 13496

RESULT 7
US-09-949-016-16790/C
Sequence 16790, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16790
LENGTH: 78630
TYPE: DNA
ORGANISM: Human
US-09-949-016-16790

Query Match 11.0%; Score 33; DB 4; Length 78630;
Best Local Similarity 57.1%; Pred. No. 4.5;
Matches 60; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 125 TCTACTAGAGTACAGAAAGCTTCAGAGATGCGGGCTGCATTCTCGAAACAGGTGT 184
DB 51895 TCTACTAGAAATACAAAATTAATGATGAGGATGTGCGAGGACCTGAGGTGCAATGAGC 51836

QY 185 TGCATTAATCAAGAAATTCCTGTGATTAACACTGTAAT 229
DB 51835 TGAGATTAGCCACATGCACTCCAACTGGGTGACAGAGAAAGACT 51791

RESULT 8
US-09-949-016-12881
Sequence 12881, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12881
LENGTH: 197336
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(197336)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12881

Query Match 11.0%; Score 33; DB 4; Length 197336;
Best Local Similarity 53.5%; Pred. No. 7.5;
Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 95 GAGCGGAGGACACCTGAAACCGCAATGCTTACTAGAGTACAGAAAGCTTCAGAGA 154
DB 89818 GGGCGGCTCTGGCGCCACCCCGCAATGTTTATTGACTGTACACAGGCTTCAGAA 89877

QY 155 TCGCGGCTGCAATTCGAAACAGGCTTGCATTAATCAAGAAATTCCTGTGGA 214
DB 89878 TCTTGAATGCTACACTTAAATAACAGAGGTTACATGAAATTCATTTCAATTCCT 89937

QY 215 TTAACACTGC 223
DB 89938 TCAGAGGC 89946

RESULT 9
US-09-949-016-14376
Sequence 14376, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;;
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;;
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 14376
;; LENGTH: 197337
;; TYPE: DNA
;; ORGANISM: Human
;;
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(197337)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14376

Query Match 11.0%; Score 33; DB 4; Length 197337;
Best Local Similarity 53.5%; Pred. No. 7.5;
Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 95 GAGCGGAGCAGACCTGAACCCGCAATGCTCTACTAGAGTACAGAAAGCCTTCAGAA 154

Db 89818 GGGCGGCTCGCGCCGCCACCCGCAATGTTTATTGACTCGTACAGGCTTCAGAA 89877

QY 155 TGGCGGGCTGCATTTCTCGAAGACGGGTGTTCGCAATTAAGAAATTCCTCTGTGA 214

Db 89878 TGTGAGTGTACTTAATAATCAGAGGTTTCACATGAATAATTCATTTTCACTTCT 89937

QY 215 TAACACTGC 223

Db 89938 TCAGAGGC 89946

RESULT 10
US-09-949-016-17272

;; Sequence 17272, Application US/09949016

;; Patent No. 6812339

;; GENERAL INFORMATION:

;; APPLICANT: VENTER, J. Craig et al.

;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

;; FILE REFERENCE: CL001307

;; CURRENT APPLICATION NUMBER: US/09/949,016

;; PRIOR FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755

;; PRIOR FILING DATE: 2000-10-20

;; PRIOR APPLICATION NUMBER: 60/237,768

;; PRIOR FILING DATE: 2000-10-03

;; PRIOR APPLICATION NUMBER: 60/231,498

;; PRIOR FILING DATE: 2000-09-08

;; NUMBER OF SEQ ID NOS: 207012

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 17272

;; LENGTH: 234288

;; TYPE: DNA

;; ORGANISM: Human

;; NAME/KEY: misc_feature

;; LOCATION: (1)...(234288)

;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17272

Query Match 11.0%; Score 33; DB 4; Length 234288;
Best Local Similarity 53.5%; Pred. No. 8.2;
Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

95 GAGCGGAGCAGACCTGAACCCGCAATGCTCTACTAGAGTACAGAAAGCCTTCAGAA 154

Db 89818 GGGCGGCTCGCGCCGCCACCCGCAATGTTTATTGACTCGTACAGGCTTCAGAA 89877

QY 155 TGGCGGGCTGCATTTCTCGAAGACGGGTGTTCGCAATTAAGAAATTCCTCTGTGA 214

Db 89878 TGTGAGTGTACTTAATAATCAGAGGTTTCACATGAATAATTCATTTTCACTTCT 89937

QY 215 TAACACTGC 223

Db 89938 TCAGAGGC 89946

RESULT 11

US-09-949-016-176915/c

;; Sequence 176915, Application US/09949016

;; Patent No. 6812339

;; GENERAL INFORMATION:

;; APPLICANT: VENTER, J. Craig et al.

;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

;; FILE REFERENCE: CL001307

;; CURRENT APPLICATION NUMBER: US/09/949,016

;; PRIOR FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755

;; PRIOR FILING DATE: 2000-10-20

;; PRIOR APPLICATION NUMBER: 60/237,768

;; PRIOR FILING DATE: 2000-10-03

;; PRIOR APPLICATION NUMBER: 60/231,498

;; PRIOR FILING DATE: 2000-09-08

;; NUMBER OF SEQ ID NOS: 207012

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 176915

;; LENGTH: 601

;; TYPE: DNA

;; ORGANISM: Human

US-09-949-016-176915

Query Match 10.9%; Score 32.6; DB 4; Length 601;
Best Local Similarity 56.2%; Pred. No. 0.43;
Matches 59; Conservative 1; Mismatches 45; Indels 0; Gaps 0;

QY 125 TCTACTAGAGTACAGAAAGCCTTCAGAGATGCGGGCTGCAATTCGAAACAGGGTCT 184

Db 369 TCTACTAATAATACAAAATTTAGTCAGCATGTGCGACGACCTGAGCTTGCACTAGC 310

QY 185 TGCATTAATCTCAAGAAATTTCTGTTGATTAACACTGTAGAAAT 229

Db 309 TGAGATTAYGCCACTGCACCTCAACCTGGGTGACAGCAAGAACT 265

RESULT 12

US-09-949-016-11868

;; Sequence 11868, Application US/09949016

;; Patent No. 6812339

;; GENERAL INFORMATION:

;; APPLICANT: VENTER, J. Craig et al.

;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

;; FILE REFERENCE: CL001307

;; CURRENT APPLICATION NUMBER: US/09/949,016

;; PRIOR FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755

;; PRIOR FILING DATE: 2000-10-20

;; PRIOR APPLICATION NUMBER: 60/237,768

;; PRIOR FILING DATE: 2000-10-03

;; PRIOR APPLICATION NUMBER: 60/231,498

;; PRIOR FILING DATE: 2000-09-08

;; NUMBER OF SEQ ID NOS: 207012

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 11868

;; LENGTH: 300598

;; TYPE: DNA

;; ORGANISM: Human

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(300598)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11868

Query Match
Best Local Similarity 10.9%; Score 32.6; DB 4; Length 300598;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 69 ACTACTCTTGTAATGTCTATTTCTAAGACGGAGCAGACCTGAAACCCGCAATGCTCTA 128
DB 49305 ATTCTTTTCCATGCTGCTTCTAAGCTCACTATCATGAAATGCCCTTGAGACATG 49364
QY 129 CTAGAAGTACAGAAAGCCTTCAGAGATGCGGGGCTGCAATTCGAAACAGGGTGTGCA 188
DB 49365 TTACAAATACATATAGCTTCCAGCTCCTCCGACATCTCGAATAATGCTGCTCCA 49424
QY 189 ATTACTCAAGAAAT 203
DB 49425 CCAACTTCATTAAGAT 49439

RESULT 13
US-09-949-016-14588
Sequence 14588, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14588
LENGTH: 302604
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(302604)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14588

Query Match
Best Local Similarity 10.9%; Score 32.6; DB 4; Length 302604;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 69 ACTACTCTTGTAATGTCTATTTCTAAGACGGAGCAGACCTGAAACCCGCAATGCTCTA 128
DB 99311 ATTCTTTTCCATGCTGCTTCTAAGCTCACTATCATGAAATGCCCTTGAGACATG 99370
QY 129 CTAGAAGTACAGAAAGCCTTCAGAGATGCGGGGCTGCAATTCGAAACAGGGTGTGCA 188
DB 99371 TTACAAATACATATAGCTTCCAGCTCCTCCGACATCTCGAATAATGCTGCTCCA 99430
QY 189 ATTACTCAAGAAAT 203
DB 99431 CCAACTTCATTAAGAT 99445

RESULT 14
US-09-949-016-14589
Sequence 14589, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14589
LENGTH: 302604
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(302604)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14589

Query Match
Best Local Similarity 10.9%; Score 32.6; DB 4; Length 302604;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 69 ACTACTCTTGTAATGTCTATTTCTAAGACGGAGCAGACCTGAAACCCGCAATGCTCTA 128
DB 99311 ATTCTTTTCCATGCTGCTTCTAAGCTCACTATCATGAAATGCCCTTGAGACATG 99370
QY 129 CTAGAAGTACAGAAAGCCTTCAGAGATGCGGGGCTGCAATTCGAAACAGGGTGTGCA 188
DB 99371 TTACAAATACATATAGCTTCCAGCTCCTCCGACATCTCGAATAATGCTGCTCCA 99430
QY 189 ATTACTCAAGAAAT 203
DB 99431 CCAACTTCATTAAGAT 99445

RESULT 15

US-09-949-016-17119
Sequence 17119, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17119
LENGTH: 308362
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(308362)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17119

Query Match
Best Local Similarity 10.9%; Score 32.6; DB 4; Length 308362;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

		Matches	71;	Conservative	0;	Mismatches	64;	Indels	0;	Gaps	0;
Qy	69	ACTACTCTGTGTAATGTCTATTCTTAAGAGCGGAGGACACCTGAACCCGCAATGTCTTA	128								
Db	99127	ATTCCCTTTCTATAGGTGCTTAAGCTCACTTATCATCAGAAATGCCCTAGAGCATG	99186								
Qy	129	CTAGAAGTACAGAAAGCCTTCAGAGATGGGGGCTGCAATTCGAAACAGGGGTGTGCA	188								
Db	99187	TTACAAATACATATAGCCTTCCCAAGCTCTCCCTGACATCCTGAAAAATTGCGTCTCA	99246								
Qy	189	ATTACTCAAGAAAT	203								
Db	99247	CCAACTTCATAAGAT	99261								

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Job time : 91.7858 secs

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OM nucleic - nucleic search, using sw model

Run on: May 4, 2005, 12:06:42 ; Search time 340.366 Seconds
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Title: US-09-300-482-619

Perfect score: 300

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Gapop 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	300	100.0	300	US-09-237-183A-276	Sequence 276, App
2	296.8	98.9	2175	US-10-425-114-33220	Sequence 33220, A
3	288.8	96.3	2737	US-10-425-115-79832	Sequence 79832, A
4	285.6	95.2	1822	US-10-425-114-2691	Sequence 2691, App
5	285.6	95.2	3088	US-10-425-114-35572	Sequence 35572, A
6	285.6	95.2	3830	US-10-425-115-79836	Sequence 79836, A
7	247.2	82.4	1937	US-10-437-963-92448	Sequence 92448, A
8	244	81.3	2696	US-10-739-930-5223	Sequence 5223, App
9	242.4	80.8	2666	US-10-437-963-92447	Sequence 92447, A
10	225.2	75.1	423	US-10-767-701-27794	Sequence 27794, A
11	218.4	72.8	1491	US-10-767-795-1472	Sequence 1472, App

12	208.8	69.6	1411	US-10-425-114-9307	Sequence 9307, App
13	208.8	69.6	2218	US-10-425-114-29640	Sequence 29640, A
14	208.8	69.6	2547	US-10-424-559-11100	Sequence 11100, A
15	197.6	65.9	1836	US-09-938-842A-1222	Sequence 1222, App
16	197.6	65.9	1836	US-09-938-842A-1222	Sequence 1222, App
17	159.8	53.3	235	US-09-237-183A-285	Sequence 285, App
18	149.2	49.7	1327	US-10-767-701-13572	Sequence 13572, A
19	145	48.3	248	US-09-237-183A-282	Sequence 282, App
20	138.4	46.1	243	US-09-237-183A-284	Sequence 284, App
21	136.4	45.5	234	US-09-237-183A-2168	Sequence 2168, App
22	131.8	43.9	296	US-09-237-183A-286	Sequence 286, App
23	124	41.3	304	US-09-237-183A-288	Sequence 288, App
24	110	36.7	288	US-09-237-183A-283	Sequence 283, App
25	110	36.7	1374	US-10-425-114-2651	Sequence 2651, App
26	107.6	35.9	1575	US-10-369-493-43763	Sequence 43763, A
27	96.6	32.2	260	US-10-437-963-92859	Sequence 92859, A
28	96.4	32.1	1551	US-10-369-493-33584	Sequence 33584, A
29	95.4	31.8	228	US-09-237-183A-287	Sequence 287, App
30	95.2	31.7	223	US-09-237-183A-2170	Sequence 2170, App
31	92	30.7	218	US-09-237-183A-2171	Sequence 2171, App
32	83.6	27.9	1251	US-10-369-493-42789	Sequence 42789, A
33	82.4	27.5	267	US-09-237-183A-278	Sequence 278, App
34	76	25.3	258	US-09-237-183A-279	Sequence 279, App
35	74	24.7	1542	US-10-369-493-32329	Sequence 32329, A
36	64	21.3	1596	US-10-369-493-26424	Sequence 26424, A
37	57.6	19.2	423	US-10-425-115-158321	Sequence 158321, A
38	52.6	17.5	362	US-09-237-183A-2182	Sequence 2182, App
39	52.4	17.5	1557	US-10-369-493-44626	Sequence 44626, A
40	38.2	12.7	205	US-09-237-183A-2169	Sequence 2169, App
41	36.2	12.1	1608	US-10-282-122A-40331	Sequence 40331, A
42	34.2	11.4	241	US-10-424-559-83869	Sequence 83869, A
43	34	11.3	579	US-09-815-242-8232	Sequence 8232, App
44	33	11.0	276820	US-10-271-416-9	Sequence 9, Appl
45	32.8	10.9	711	US-10-001-254-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-09-237-183A-276
Sequence 276, Application US/09237183A
Publication No. US20030135870A1
GENERAL INFORMATION:
APPLICANT: Cheikh, No. US20030135870A1dine
APPLICANT: Fisher, Dane K.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
FILE REFERENCE: 38-21 (15089)B
CURRENT APPLICATION NUMBER: US/09/237,183A
PRIOR FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: US 60/067,000
NUMBER OF SEQ ID NOS: 2814
SEQ ID NO 276
LENGTH: 300
TYPE: DNA
ORGANISM: Zea mays
US-09-237-183A-276

Query Match 100.0%, Score 300, DB 10, Length 300;
Best Local Similarity 100.0%, Pred. No. 2.1e-89;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATTATTGACACACCCGATCTGCTGGATTGATCATCAATTTCTCAACTAGACCTG 60
DB 1 GATTATTGACACACCCGATCTGCTGGATTGATCATCAATTTCTCAACTAGACCTG 60
QY 61 AACTGCAACTCTCTTGTATTTGATTTTCAAGGCGAGGACACCTGAAACCCGCA 120
DB 61 AACTGCAACTCTCTTGTATTTGATTTTCAAGGCGAGGACACCTGAAACCCGCA 120

QY	121	ATGCTCTACTCTGAAATGACAGAAAGCCCTTCAGAGATCGCGGGCTGCATCTCTCGAACAAG	180
Db	121	ATGGCTACTACTAGAAATGACAGAAAGCCCTTCAGAGATCGCGGGCTGCATCTCTCGAACAAG	180
QY	181	GTGTGCAATTAATCTCAAGAAAATCTCTGTGTGATTAACACTGCTAGAGAAATAGAGGATGCT	240
Db	181	GTGTGTCAATTAATCTCAAGAAAATCTCTGTGTGATTAACACTGCTAGAGAAATAGAGGATGCT	240
QY	241	TAGCTCGGTTTCTATGTTTGAATGGGTTGGGCGTAGACATTCAAGAAATGTCTGTGTGG	300
Db	241	TAGCTCGGTTTCTATGTTTGAATGGGTTGGGCGTAGACATTCAAGAAATGTCTGTGTGG	300

RESULT 2

```

US-10-425-114-33220
; Sequence 33320: Application US/10425114
; Publication No. US20040034868A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 33220
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZWFLMO17077A12_FLI
; US-10-425-114-33220

```

Query Match

	Best Local Similarity	99.3%	Pred. No. 6.7e-86;	Matches 298;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	GATTATTGACAAACCGGATCTTGCGGATGATCATCAAAATGGCTCACTAGGACCTG	60					
Db	768	GATTATTGACAAACCGGATCTTGCGGATGATCATCAAAATGGCTCACTAGGACCTG	827					
QY	61	AACGCGCACTACCTCTTGTAATTGTCACTTTCTTAAGCGCGAGGCACACTGAAACCGCA	120					
Db	828	AACGCGCACTACCTCTTGTAATTGTCACTTTCTTAAGCGCGAGGCACACTGAAACCGCA	887					
QY	121	ATGGCTACTAGAGTACAGAAAGCCTTCAGAGATCGGGGGCTGCAATTCTGAAACAG	180					
Db	888	ATGGCTACTAGAGTACAGAAAGCCTTCAGAGATCGGGGGCTGCAATTCTGAAACAG	947					
QY	181	GTCGTTGCAATTACCAAGAAATTTCTGTGTGATACCTGCTGAATAGAGGATGT	240					
Db	948	GTCGTTGCAATTACCAAGAAATTTCTGTGTGATACCTGCTGAATAGAGGATGT	1007					
QY	241	TAGCTCGGTTTCCATATTTGATTTGGGTGGTGGATCAAAATGTCCTGTGTGG	300					
Db	1008	TAGCTCGGTTTCCATATTTGATTTGGGTGGTGGATCAAAATGTCCTGTGTGG	1067					

RESULT 3

US-10-425-115-79832
Sequence 79832, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```

; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 79832
; LENGTH: 2737
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: clone ID: MRT4577_172832C.1
; US-10-425-115-79832

```

Query Match

[illegible]

RESULT 4

```

US-10-425-114-2691
Sequence 2691, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 2691
LENGTH: 1822
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: clone ID: 700221523_FLI
US-10-425-114-2691

```

Query

Best Local Similarity 97.0%; Pred No. 3.3e-84;
Mismatch 0; Indels 0; Gaps 0;
Total 291; Conservative 9;

1 GATTATGACACACCGATCCGTCGGATGATGATCATTAATTGCTCAACTGAGACTG 60
430 GATTATGACACACGATCCGTCGGATGATGATCATTAATTGCTCAACTGAGACTG 489
61 AACGCGAACTACTCTTGTATATGTCATTTCTTAAGCGGAGGACACCTGAAACCGCA 120

Db	490	AACTCGCACTACTCTTGTAATGTGATCTTAAAGAGGAGGACACCTGAACCCGA	5439
Qy	121	ATGCTCTACTAGAAATGACAGAAAGCCTTCAGAGATCGGGGCTGCATTTCTCGAAACAG	180
Db	550	ATGGGCTACTCGAATGACAGAAAGCCTTCAGAGATCGGGGCTGCATTTCTCGAAACAG	609
Qy	181	GTGTTCATTTCTCGAAGAAATTCCTCGTTGGATACACATGCTAGAAATGAGGAGTGT	240
Db	610	GTGTTCATTTCTCGAAGAAATTCCTCGTTGGATACACATGCTAGAAATGAGGAGTGT	669
Qy	241	TAGCTCGATTTCCATGATTGATGGGGTGGGTGATGACATTCAGAAATGTCTCTGTG	300
Db	670	TAGCTCGATTTCCATGATTGATGGGGTGGGTGATGACATTCAGAAATGTCTCTGTG	729

```

US-10-425-114-35572
RESULT 5
US-10-425-114-35572
; Sequence 35572, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 35572
; LENGTH: 3088
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMR0B73058A09_FLI
US-10-425-114-35572

```

Query Match	95.2%	Score 285.6	DB 17	Length 3088
Best Local Similarity	97.0%	Pred. No. 4.3e-84		
Matches 291	Conservative 0	Mismatches 9	Indels 0	Gaps 0
Qy	1	GATTATTTGACAAACCGATCCTGCTGGGATTTGATCATCAATTGCTCAACTAGGACCTG	60	
Db	712	GATTATTGACAAACCGATCTCTGGGATTTGATCATCAAAATTCTCACTAGGACCTG	771	
Qy	61	AAC TGGAAC TACTCTTG TAA TTG CATTTCTA AGAGG GGA GGCACAC CTGAA ACCGCA	120	
Db	772	AAC TGGAAC TACTCTTG TAA TTG CATTTCTA AGAGG GGA GGCACAC CTGAA ACCGCA	831	
Qy	121	ATG GTC TAC TAA GAG TAC AAG CTT CAG AGA TG CGG GGC TGC AAT TCT CGA A A CAG	180	
Db	832	ATG GGC TAC TCG AAG A G TAC AAG AAG CTT CAG AGA TG CAG GTC TGC AAT TCT CGA A A CAG	891	
Qy	181	G TGT TGA CAT TAC TCA GAA AAT TCT CTT GTG A TAA CAC TGC TTA GAT TAA GAG GA TGT	240	
Db	892	G TGT TGA CAT TAC TCA GAA AAT TCT CTT GTG A TAA CAC TGC CCA TGA GAG GAT GT	951	
Qy	241	TAG CTG GAT TCC ATG TTT GAT TGG GTG GAG GAG CTT CAG AAT GTCTG CTG G	300	
Db	952	TAG CTG GAT TCC ATG TTT GAT TGG GTG GAG GAG CTT CAG AAT GTCTG CTG G	1011	

RESULT 6
US-10-425-115-79836
Sequence 79836, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: KOVALLIC, David K.
APPLICANT: Zhou, Yihua

```

APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 79836
LENGTH: 3830
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_172836C.1
US-10-425-115-79836

```

	Query Match	95.2%	Score 285.6	DB 18	Length 3830	
	Best Local Similarity	97.0%	Pred. No. 4.8e-84			
	Matches 291	Conservative 0	Mismatches 9	Indels 0	Gaps 0	
Qy	1	GATTATTTGCAACACCCGATCTCGTGGATTTGATATCAATTTGCTCAACTAGACCTG	60			
Db	1452	GATTATTTGCAACACCCGATCTCGTGGATTTGATATCAATTTGCTCAACTAGACCTG	1511			
Qy	61	AAC TGGCAACTACTCTTGTATTTGTCAATTTCTAAGACGAGGACACCTGAAACCCGCA	120			
Db	1512	AAC TGGCAACTACTCTTGTATTTGTCAATTTCTAAGACGAGGACACACCTGAAACCCGCA	1571			
Qy	121	ATG GTC TACTAGAAATACAGAAAGCTTTACAGACATGCGGGCTGCAATTCTCGAAACAGG	180			
Db	1572	ATG G G C T A C T A G A A G T A C A G A A A G C T T T C A G A G A T G C A G G C T T C G A A A T T C T C G A A A C A G G	1631			
Qy	181	G T G T T G C A A T T A C T C A G A A A A A T T C T G T T G G A T T A C A C T G C T A G A A T T A G A G G A T G G T	240			
Db	1632	G T G T T G C A A T T A C T C A G A A A A A T T C T G T T G G A T T A C A C T G C C A G A A T T A G A G G A T G G T	1691			
Qy	241	T A G C T G G A T T T C C A T A T T T G A T T G G G T G G T A G A C T T C A G A A A T G C T G C T G G G	300			
Db	1692	T A G C T G G A T T T C C A T A T T T G A C T G G G T G G T A G A C T T C A G A A A T G C A C T G T T G	1751			

```

RESULT 7
US-10-437-963-92448/c
? Sequence 92448, Application US/10437963
? Publication No. US2004012343A1
? GENERAL INFORMATION:
? APPLICANT: La Rosa, Thomas J.
? APPLICANT: Kovalic, David K.
? APPLICANT: Zhou, Yihua
? APPLICANT: Cao, Yongwei
? APPLICANT: Wu, Wei
? APPLICANT: Boukharov, Andrey A.
? APPLICANT: Barbazuk, Brad
? APPLICANT: Li, Ping
? TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
? FILE REFERENCE: 38-21(53221)B
? CURRENT FILING DATE: 2003-05-14
? NUMBER OF SEQ ID NOS: 204966
? SEQ ID NO 92448
? LENGTH: 1937
? TYPE: DNA
? ORGANISM: Oryza sativa
? FEATURE:
? OTHER INFORMATION: Clone ID: PAT_MRT4530_90929C.1
US-10-437-963-92448

```

Query Match	82.4%	Score 247.2	DB 18	Length 1937
Best Local Similarity	89.0%	Pred. No. 2.2e-71		
Matches 267	Conservative 0	Mismatches 33	Indels 0	Gaps 0
OY	1	GATTATTGACAAACCGATTCCTCTGGAGTATATCATCAATATGCTCACTAGAGCTG	60	

Db 1139 GATTATTGACAACACTGATCTGTGTAATGACCATCAAAATGGCTCACTAGACACG 1080
QY 61 AACTGGCACTACTCTTGTATTTGTATTTCTTAAGACCGAGCAACCTGAAACCCGCA 120
Db 1079 AGCTTCACTACTCTGTATTTGTATTTCTTAAGATGAGGACACCTGAAACCCGCA 1020
QY 121 ATGGCTACTAGAAAGTACAGAAAGCCTTCAGAGATGCGGGCTGCAATTCGTGAAACAG 180
Db 1019 ATGGCTGTGTAAGTACAGAAAGCCTTCAGAGATGCGGGCTGCAATTCGTGAAACAG 960
QY 181 GTGTTCGAATTAATCAAGAAATTTCTGTGTGATTAACCTGCTAGAAATAGAGGATGT 240
Db 959 GAGTTGCACTACTCAAGAAATTTCTGTGTGATTAACCTGCTAGAAATAGAGGATGT 900
QY 241 TAGCTCGTTTCTTATTTGATTTGGTTGGTGTGAGTCACTTCAAAATCTGCTGTG 300
Db 899 TAGCTGATTTTCCATGTTTGAATGGGTTGGTGAAGAACATCAAGAAATGTCACTGTG 840

RESULT 8

US-10-739-930-5223
Sequence 5223, Application US/10739930
Publication No. US20040216190A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 5223
LENGTH: 2696
TYPE: DNA

ORGANISM: Triticum aestivum
FEATURE:

OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER693_1
US-10-739-930-5223

Query Match

Best Local Similarity 81.3%; Score 244; DB 18; Length 2696;
Matches 265; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 GATTATTGACAACACCGATCTGTGATTCATCAAAATGCTCACTAGACCTG 60
Db 1083 GATTATTGACAACACCGATCTGTGATTCATCAAAATGCTCACTAGACCTG 1142
QY 61 AACTGGCACTACTCTTGTATTTGTATTTCTTAAGACCGAGCAACCTGAAACCCGCA 120
Db 1143 AACTGGCACTACTCTTGTATTTGTATTTCTTAAGACCGAGCAACCTGAAACCCGCA 1202
QY 121 ATGGCTACTAGAAAGTACAGAAAGCCTTCAGAGATGCGGGCTGCAATTCGTGAAACAG 180
Db 1203 ATGGCTACTAGAAAGTACAGAAAGCCTTCAGAGATGCGGGCTGCAATTCGTGAAACAG 1262
QY 181 GTGTTCGAATTAATCAAGAAATTTCTGTGTGATTAACCTGCTAGAAATAGAGGATGT 240
Db 1263 GTGTTCGAATTAATCAAGAAATTTCTGTGTGATTAACCTGCTAGAAATAGAGGATGT 1322
QY 241 TAGCTCGTTTCTTATTTGATTTGGTTGGTGTGAGTCACTTCAAAATCTGCTGTG 300
Db 1323 TAGCTCGTTTCTTATTTGATTTGGTTGGTGTGAGTCACTTCAAAATCTGCTGTG 1382

RESULT 9

US-10-437-963-92447/c
Sequence 92447, Application US/10437963
Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bardazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 92447
LENGTH: 2666
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_90928C.1
US-10-437-963-92447

Query Match 80.8%; Score 242.4; DB 18; Length 2666;
Best Local Similarity 88.0%; Pred. No. 1e-69; Indels 0; Gaps 0;
Matches 264; Conservative 0; Mismatches 36;

QY 1 GATTATTGACAACACCGATCTGTGATTCATCAAAATGCTCACTAGACCTG 60
Db 1862 GATTATTGACAACACCGATCTGTGATTCATCAAAATGCTCACTAGACCTG 1803
QY 61 AACTGGCACTACTCTTGTATTTGTATTTCTTAAGACCGAGCAACCTGAAACCCGCA 120
Db 1802 AACTGGCACTACTCTTGTATTTGTATTTCTTAAGACCGAGCAACCTGAAACCCGCA 1743
QY 121 ATGGCTACTAGAAAGTACAGAAAGCCTTCAGAGATGCGGGCTGCAATTCGTGAAACAG 180
Db 1742 ATGGCTACTAGAAAGTACAGAAAGCCTTCAGAGATGCGGGCTGCAATTCGTGAAACAG 1683
QY 181 GTGTTCGAATTAATCAAGAAATTTCTGTGTGATTAACCTGCTAGAAATAGAGGATGT 240
Db 1682 GAGTTGCACTACTCAAGAAATTTCTGTGTGATTAACCTGCTAGAAATAGAGGATGT 1623
QY 241 TAGCTCGTTTCTTATTTGATTTGGTTGGTGTGAGTCACTTCAAAATCTGCTGTG 300
Db 1622 TAGCTCGTTTCTTATTTGATTTGGTTGGTGTGAGTCACTTCAAAATCTGCTGTG 1563

RESULT 10

US-10-767-701-27794
Sequence 27794, Application US/10767701
Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53335)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 27794
LENGTH: 423
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: 721656
US-10-767-701-27794

Query Match 75.1%; Score 225.2; DB 18; Length 423;
Best Local Similarity 98.7%; Pred. No. 2.2e-64;
Matches 227; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATTATTGACAACACCGATCTGTGATTCATCAAAATGCTCACTAGACCTG 60
Db 194 GATTATTGACAACACCGATCTGTGATTCATCAAAATGCTCACTAGACCTG 253

QY	Db	QY	Db
6	120	121	180
AACTGGCACTCTCTGTAATTGCAATTTCAAGAGGAGGAGCAACCTGAAACCCGA		ATGCTTACTAGAAAGTACAGAAAGCCTCAGAGATGCGGGCTGCAATTCGAAACAGG	
254	313	314	373
AACTGGCACTCTCTGTAATTGCAATTTCAAGAGGAGGAGCACTGAAACCCGA		ATGCTTACTAGAAAGTACAGAAAGCCTCAGAGATGCGGGCTGCAATTCGAAACAGG	
181	230		
GTTTGCATTACTCAGAAATTTCTCTGTGGATPAACCTGCCAAGTA	423		

```

RESULT 11
US-10-767-795-1472
; Sequence 1472, Application US/10767795
; Publication No. US20040181830A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53534)B
; CURRENT APPLICATION NUMBER: US/10/767,795
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 1471
; LENGTH: 1491
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURES:
; OTHER INFORMATION: Clone ID: GOSH1-09MAY01-C1260_1
; US-10-767-795-1472

```

Query Match	72.8%	Score 218.4;	DB 18;	Length 1491;
Best Local Similarity	83.0%	Pred. No. 7.8e-62;		
Matches 249;	Conservative 0;	Mismatches 51;	Indels 0;	Gaps 0

Qy	1	GATTATTACACAACCCGATCTCGCGGATATGATCATCAATAATGCTCAATAGACCTG	60
Db	71	GATTATTGATTAACAGATCTCGCTGGAATGATCATCAATAATAGACAACTTGGGCTG	130
Qy	61	AACTCGCAACTACTCTTGTAATTCATTTCTTAAGCGGAGGCAACCTGAACCCGCA	120
Db	131	AGTGGCTTCTACTCTTGTAATTCGATTTCAAAAGTGGAGGTAAACCTCGAAACAAGAA	190
Qy	121	ATGCTCTACAGAGATGACAGAAAGCCTCAGAGATCGGGGCTCAATTCGCAAAAGG	180
Db	191	ATGCTCTATTGGAGTACAGAAAGCCTTCGGAAGCTGGTCTGGATTTGCAAAACAGG	250
Qy	181	GTGTTCCAATTACTCAGAAAATTTCTGTGTGATTAACACTGTAGATAGAGGATGCT	240
Db	251	GTGTTCCTAATACACAGAAAATTTCTGTGTGACAACTGCAAGATTAGGGTTGGG	310
Qy	241	TACCTGGTTTCTATGTTTGATTTGGGTGGTGGTAGACATTCAGAAATGTCTGCTGG	300
Db	311	TACCAAGTTCCTATGTTTGATTTGGGTGGGAGGACCTCGAATAATGCTCTCACTTG	370

RESULT 12
 US-10-425-114-9307
 ; Sequence 9307, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

```

; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 9307
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700845275_FLI
; US-10-425-114-9307

```

	Query Match	Best Local Similarity	69.6%;	Score 208.8;	DB 17;	Length 1411;				
	Matches	243;	Conservative	0;	Mismatches	57;	Indels	0;	Gaps	0;
QY	1	GATTATTGCAACACCGATCTCTGCTGGGATTGATCATCAAAATTGCTCAACTGAGACTG	60							
Db	24	GATTGTGGACAACACGGATCTCTGGGAATTGATCATCAAGATTGCAACACTGGGGCTG	83							
QY	61	AAC TGCAACTACTCTCTGTGTAATTGTCATTTCTTAAGACGGAGCACACTGMAACCCGCA	120							
Db	84	AGCTAGCTTCAACACTTGTGATTGTGATTCAAAGATGGAGGTACTCTGAGACGAA	143							
QY	121	ATGCTCTACTAGAAAGTACAGAAAAGCCTTCAGAAATGGGGGCTGCATTTCTCGAAAACAG	180							
Db	144	ATGGTTTATTGGAAGTGCAGAAAGCCTTTGTGTAAAGCAGGCTTGATTTTCTTAAACAG	203							
QY	181	GCTGTGCAATTACTCAAGAAAATTTCTCTGTTGGATTAACATGCTAGAAATAGAGGATGCT	240							
Db	204	GTGTGCTATTAAACAAGAAAATCTTTGTTGGATTAACATGCTAGAAATAGAGGCTGCT	263							
QY	241	TAGCTGCGTTTCCATGCTTTGATTGGTGTGCTGAGCACTTCAAGAAATGTCGCTGTG	300							
Db	264	TAGCTAAATTTCCATGCTTTGATTGGTGTGAGGTAAAGCTCAGAAATGCTGCACTTG	323							

RESULT 13

US-10-425-114-29640
; Sequence 29640, Application US/10425114
; Publication No. US20040034888A1

APPLICANT: Liu, Jindong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 23640

OTHER INFORMATION: CLONE ID: UC-GMFLMINSOY100E04_FLI
US-10-425-114-29640

Query Match	69.64;	Score 208.8;	DB: 17;	length 2218;
Best Local Similarity	81.08;	Pred. No. 1.5e-58;		
Best Match 243; Conservative	0;	Mismatches 57;	Indels 0;	Gaps 0;

Qy	Db	Qy	Db
1	775	61	835
GATTATTTGCAACACCGATCTCGTGGATATCATCAAAATTTGCTCACTTGGACCTG	GATTTTGGACCAACCGATCTCGTGGATTTGATCATCAGATTGCACAACTTGGGGCTG	AACCTGGCAACTACTCTTGTATTTGTCACTTTCTAAGACGGAGCACACTCTGAAAACCCGCA	AGCTAGCTTTCAACACTTGTATTTGTGTATTTCAAGATGAGAGTACTCTTGAGACCGAAA
60	834	120	894

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QY 121 ATGCTACTAGAGTACAGAAAGCCCTTCAGAGATGGGGGCTGCAATTCTCGAAACAG 180
DB 895 ATGCTTTATGGAAGTGCAGAAAGCCCTTCGTGAGAGAGCCCTTGAAATTTCTTAACAG 954
QY 181 GTGTGCAATTACTCAAGAAATTTCTGTGTGATTAACACTGCTAGAAATAGAGGATGT 240
DB 955 GTGTGCTATTAACAGAAATTTCTTTGTGTGATTAACACTGCAAGATTTAGAGGCTGT 1014
QY 241 TAGCTGGTTTCTATGTTGATTTGGTTGGTGTAGAGACTTCAAGAAATGCTGTGTG 300
DB 1015 TAGCTAGATTTCTATGTTGATTTGGTTGGTGTAGAGACTTCAAGATGCTGTGAGTTG 1074

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RESULT 14

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US-10-424-599-11100
; Sequence 11100, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongmei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 11100
; LENGTH: 2547
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(2547)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110030C.1
US-10-424-599-11100

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Query Match      69.6%; Score 208.8; DB 17; Length 2547;
Best Local Similarity 81.0%; Pred. No. 1.6e-58;
Matches 243; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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QY 1 GATTATTGACAAACCCGATCCTGCTGAGATTGATCATCAAAATGCTCAACTAGAGCCGTG 60
DB 1022 GATTGTGGACAACCGGATCCTGCTGGAATTGATCATCAATTCGACAACTTGGGCTTG 1081
QY 61 AACTGGCACTACTCTTGTAAATTTGTCATTTCTAAGACGGAGGCAACCTGAAACCCGCA 120
DB 1082 AGCTGAGCTTCAACACTTGTGATTTGATATCAAAAGTGGAGTACTCTCTGAGACAGAA 1141
QY 121 ATGGCTACTAGAGTACAGAAAGCCCTTCAGAGATCGGGGCTGCAATTTCTGAAACAG 180
DB 1142 ATGGTTATTTGGAATGTCAGAAAGCCCTTCGTGAAGCAGGCTTGGATTTCTTAACAG 1201
QY 181 GTGTGCAATTACTCAAGAAATTTCTGTGTGATTAACACTGCTAGAAATAGAGGATGT 240
DB 1202 GTGTGCTATTAACAGAAATTTCTTTGTGTGATTAACACTGCAAGATTTAGAGGCTGT 1261
QY 241 TAGCTGGTTTCTATGTTGATTTGGTTGGTGTAGAGACTTCAAGAAATGCTGTGTG 300
DB 1262 TAGCTAGATTTCTATGTTGATTTGGTTGGTGTAGAGACTTCAAGATGCTGTGAGTTG 1321

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RESULT 15

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US-09-938-842A-1222
; Sequence 1222, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel

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; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1222
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1222

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Query Match      65.9%; Score 197.6; DB 9; Length 1836;
Best Local Similarity 78.7%; Pred. No. 7.6e-55;
Matches 236; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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QY 1 GATTATTGACAAACCCGATCCTGCTGAGATTGATCATCAAAATGCTCAACTAGAGCCGTG 60
DB 641 GATTATTGACAAACCCGATCCTGCTGAGATTGATCATCAATTCGACAACTTGGGCTAG 700
QY 61 AACTGGCACTACTCTTGTAAATTTGTCATTTCTAAGACGGAGGCAACCTGAAACCCGCA 120
DB 701 AGCTGGCTCGACCTTATGATTTGTCATCTCAAGAGTGGAGTACTCTGAAACTAGAA 760
QY 121 ATGGCTACTAGAGTACAGAAAGCCCTTCAGAGATCGGGGCTGCAATTTCTGAAACAG 180
DB 761 ATGGACTACTGAAAGTGCAGAAAGCATTCGCTGAAGCTGTCTGAATTTCCCAAAACAG 820
QY 181 GTGTGCAATTACTCAAGAAATTTCTGTGTGATTAACACTGCTAGAAATAGAGGATGT 240
DB 821 GTGTGCAATTACTCAAGAAATTTCTGTGTGATTAACACTGCTAGAAATAGAGGATGT 880
QY 241 TAGCTGGTTTCTATGTTGATTTGGTTGGTGTAGAGACTTCAAGAAATGCTGTGTG 300
DB 881 TAGCTAGATTTCTATGTTGATTTGGTTGGTGTAGAGACTTCAAGATGCTGTGAGTTG 940

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Search completed: May 4, 2005, 21:11:52
Job time : 341.366 secs

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